

Gencore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:39:34 ; Search time 2651 Seconds  
(without alignments)  
10727.712 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359  
Sequence: 1 atggaacccctcccgagtc.....agtccttcagaagatga 1359

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 30

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:\*

1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
------------	-------------	-------	--------	----	----	-------------

c	1	55	4.0	86743	8	AP003218
---	---	----	-----	-------	---	----------

AP003218 Oryza sat

## ALIGNMENTS

RESULT 1  
AP003218/c  
LOCUS AP003218 86743 bp DNA linear PLN 19-DEC-2001  
DEFINITION Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJNB0021A09,  
complete sequence.

ACCESSION AP003218  
VERSION AP003218.3 GI:17933033  
KEYWORDS HTG.  
SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:OSJNB0021A09.  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 86743)  
Sasaki, T., Matsumoto, T. and Yamamoto, K.

AUTHORS Direct Submission  
TITLE Submitted (19-FEB-2001) Takuji Sasaki, National Institute of  
JOURNAL Agrobiological Sciences, Rice Genome Research Program; Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
On Dec 18, 2001 this sequence version replaced gi:17132514.  
The orientation of the sequence is from -21M13 to M13rev of the BAC  
clone.

## COMMENT

FEATURES  
source Location/Qualifiers

1..86743  
/organism="Oryza sativa"  
/cultivar="Nipponbare"  
/db\_xref="taxon:4530"  
/chromosome="1"  
/clone="OSJNB0021A09"

BASE COUNT 24257 a 19182 c 18802 g 24502 t  
ORIGIN

Query Match 4.0%; Score 55; DB 8; Length 86743;  
Best Local Similarity 100.0%; Pred No. 1.3e-19;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 820 GGATTTCAAGACCACTAATAATTGCTTGATGCTCTACTCTCTTTGGCAGG 874  
|||||  
DB 55073 GGATTTCAAGACCACTAATAATTGCTTGATGCTCTACTCTTTGGCAGG 55019

Search completed: November 1, 2002, 17:08:24  
Job time : 2683 secs

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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 14:20:34 ; Search time 251 Seconds  
(without alignments)  
9295.963 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359  
Sequence: 1 atgaccctcccccgcagtc.....agttcttcgagaagatga 1359

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 30

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_032802:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1359	100.0	1359	21	AAZ51791
2	62	4.6	1031	21	AAZ51792

ALIGNMENTS

RESULT 1  
AAZ51791

ID	AAZ51791 standard; cDNA; 1359 BP.
XX	
AC	AAZ51791;
XX	
DF	04-JUL-2000 (first entry)
XX	
DE	Corn farnesyltransferase beta subunit cDNA.
XX	
KW	Corn; farnesyltransferase beta subunit; transgenic plant;
KW	drought tolerance; cell growth; ss.
XX	
OS	Zea mays.
XX	
XX	
FT	Key Location/Qualifiers
FT	CDS 1..1359
FT	/tag= a
FT	/product= "Farnesyltransferase beta subunit"
XX	
PN	W0200014207-A2.
XX	
PD	16-MAR-2000.
XX	
PF	07-SEP-1999; 99MO-US20419.
XX	
PR	08-SEP-1998; 98US-0099521.
XX	
PA	(DUPD ) DU PONT DE NEMOURS & CO E I.
XX	
PI	Cahoon RE, Miao G, Powell W;
XX	
DR	WPI, 2000-256964/22.
DR	P-PSDB: AAT70502.
XX	
PT	New isolated polynucleotide encoding farnesyltransferase polypeptide is useful for producing transgenic plants with an altered level of farnesyltransferase -
PT	
XX	
PS	Claim 3; Page 38-39; 51pp; English.
XX	
CC	The present sequence is a cDNA encoding farnesyltransferase beta subunit from clone p0127.entbu.18r isolated from corn nucellus tissue
CC	cDNA library. The present sequence is used in the construction
CC	of a chimeric gene to produce transgenic plants with altered level
CC	of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC	activity may have enhanced tolerance to drought stress. Nucleic acids
CC	encoding all or a part of farnesyltransferase proteins can be used in
CC	studies to understand cell growth in plants and provide genetic tools to
CC	control cell growth and improve tolerance to drought in mature plants.
XX	
SQ	Sequence 1359 BP; 340 A; 308 C; 351 G; 360 T; 0 other:
XX	
Query Match	100.0%; Score 1359; DB 21; Length 1359;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1359;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGACCCCTCCCTCCCGAGTCGACGCCGCCGACGAGACGCCGCGGCGGAT 60
DB	
DB	1 ATGACCCCTCCCTCCCGAGTCGACGCCGCCGACGAGACGCCGCGGCGGAT 60
QY	61 CCCGACCTACCGAGGCTCACGGTACGACGAGTGAGACATGAAAGTGAGGCGCAGGTT 120
DB	
DB	61 CCCGACCTACCGAGGCTCACGGTACGACGAGTGAGACATGAAAGTGAGGCGCAGGTT 120
QY	121 GCGACATCTACCGCTCCCTTCGGGGCGCGCCCAACAAGAAATCCATCATGCTAGAG 180
DB	
DB	121 GCGACATCTACCGCTCCCTTCGGGGCGCGCCCAACAAGAAATCCATCATGCTAGAG 180
QY	181 CTGTGGCGTGATCAGCATATCGATCTGACCGCTGGGCTGAGCGATATGGACACGCC 240
DB	
DB	181 CTGTGGCGTGATCAGCATATCGATCTGACCGCTGGGCTGAGCGATATGGACACGCC 240
QY	241 TTTCATGTTCTAGATGCATCGCCCTTGGCTATGCTACTAGTGATGTTCACTGCTGT 300
DB	
DB	241 TTTCATGTTCTAGATGCATCGCCCTTGGCTATGCTACTAGTGATGTTCACTGCTGT 300

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Db 241 TTTCATCTTCTAGATGCCAATCGCCCTTGGCTATGCTACTGGATGGTTCAATCCACTTTCCT 300
QY 301 TTGCTGATGAAGCACTTGATGATCTTGAGAATGATATCATAGACTTCTTAGCTGCA 360
Db 301 TTGCTGATGAAGCACTTGATGATCTTGAGAATGATATCATAGACTTCTTAGCTGCA 360
QY 361 TGTGAGATTAAGATGGTGGATATAGTGGTGAGACTGGACAGTTGGCTCAACCTAGTACG 420
Db 361 TGTGAGATTAAGATGGTGGATATAGTGGTGAGACTGGACAGTTGGCTCAACCTAGTACG 420
QY 421 ACCTATGCTGCTGTAATTAACATGTCACAATAGGGAGCGAAGAGAGATTTGATCATATC 480
Db 421 ACCTATGCTGCTGTAATTAACATGTCACAATAGGGAGCGAAGAGAGATTTGATCATATC 480
QY 481 AATAGGGCAACCTGTACAAATTTATGCTCAGATGAAGATGTATCAGCTGCTTTCAGA 540
Db 481 AATAGGGCAACCTGTACAAATTTATGCTCAGATGAAGATGTATCAGCTGCTTTCAGA 540
QY 541 ATGCATGATGCTGGCGAATTTGATGTCGGTCTTCTTACACCGCTATATCGCTTGGCAGC 600
Db 541 ATGCATGATGCTGGCGAATTTGATGTCGGTCTTCTTACACCGCTATATCGCTTGGCAGC 600
QY 601 CTTCGTGAATATCTCTGATTTTAACTGCGCAAAAGCTAGCGGCACTACATAGCAAGATGT 660
Db 601 CTTCGTGAATATCTCTGATTTTAACTGCGCAAAAGCTAGCGGCACTACATAGCAAGATGT 660
QY 661 CAAACTTATAGAGTGTGATTTGCTGGGAGCCCTTATGCTGAGACATGCTGGCTATACA 720
Db 661 CAAACTTATAGAGTGTGATTTGCTGGGAGCCCTTATGCTGAGACATGCTGGCTATACA 720
QY 721 TTCTGTGATTTGCTGCTTTTGTGATTCCTGTAATGAGGCGAGAGAAAGTTGACTTGGCTAGT 780
Db 721 TTCTGTGATTTGCTGCTTTTGTGATTCCTGTAATGAGGCGAGAGAAAGTTGACTTGGCTAGT 780
QY 781 TTGATTTGGGCTGGGCTTTTTCGTCAGAGAGTGAATGCGGATTTTCAAGAGACGACATAT 840
Db 781 TTGATTTGGGCTGGGCTTTTTCGTCAGAGAGTGAATGCGGATTTTCAAGAGACGACATAT 840
QY 841 AAATTTGTTGATGCTTCTCTCTTTTGGCAGAGAGCTCCATTTGCTTTCACACAAG 900
Db 841 AAATTTGTTGATGCTTCTCTCTTTTGGCAGAGAGCTCCATTTGCTTTCACACAAG 900
QY 901 TTTAATTACGATTTGTTGTAAGCAATTAAGTCTCTGTAATTCCTGCAAAAGGCCATCAGA 960
Db 901 TTTAATTACGATTTGTTGTAAGCAATTAAGTCTCTGTAATTCCTGCAAAAGGCCATCAGA 960
QY 961 GAGGATCCGTCAGACACACAGTTCATATGCGGTCACCGCGAAGAAAGTCTCTGCGCTG 1020
Db 961 GAGGATCCGTCAGACACACAGTTCATATGCGGTCACCGCGAAGAAAGTCTCTGCGCTG 1020
QY 1021 GACTATGCGAAGTTTGGATTTGATTTTATCAACAGAGACAACCAAAATTTGGCCCACTCTTC 1080
Db 1021 GACTATGCGAAGTTTGGATTTGATTTTATCAACAGAGACAACCAAAATTTGGCCCACTCTTC 1080
QY 1081 CATTAACATTTGCTCTGCAACATACATCTTCTCTAGGTACTAGAGAGGCGCTTG 1140
Db 1081 CATTAACATTTGCTCTGCAACATACATCTTCTCTAGGTACTAGAGAGGCGCTTG 1140
QY 1141 AGGATTAAGCCTGGAAGAAAGACAGATCAGTATCATGCTCTGCGCTCAGGCGCTC 1200
Db 1141 AGGATTAAGCCTGGAAGAAAGACAGATCAGTATCATGCTCTGCGCTCAGGCGCTC 1200
QY 1201 GCAGTTAGCCAGTACATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1201 GCAGTTAGCCAGTACATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 CTTCGACCGTACTCTAATTTGCTGAGCCCAATTCATCTTACAAATGTTTGTCTAGAT 1320
Db 1261 CTTCGACCGTACTCTAATTTGCTGAGCCCAATTCATCTTACAAATGTTTGTCTAGAT 1320
QY 1321 AAGTACCATACAGCTATGAGTTCTTCTCAGAAAGATGA 1359
Db 1321 AAGTACCATACAGCTATGAGTTCTTCTCAGAAAGATGA 1359

```

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RESULT 2
AA251792
ID AA251792 standard; cDNA; 1031 BP.
XX
AC AA251792:
XX
DT 04-JUL-2000 (first entry)
XX
DE Rice farnesyltransferase beta subunit cDNA.
XX
KW Rice; farnesyltransferase beta subunit; transgenic plant;
XX drought tolerance; cell growth; ss.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT CDS 91..1029
FT FT /*tag= a
FT FT /product= "Farnesyltransferase beta subunit"
FT FT /note= "Does not include stop codon"
FT FT /partial
XX
PN WO200014207-A2.
XX
PD 16-MAR-2000.
XX
PE 07-SEP-1999; 99MO-US20419.
XX
PR 08-SEP-1998; 98US-0099521.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon RE, Miao G, Powell W;
XX WPI: 2000-256964/22.
XX DR P-PSDB: AAY70503.
XX
PT New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT useful for producing transgenic plants with an altered level of
PT farnesyltransferase -
XX
PS Claim 3; Page 40-41; 51pp; English.
XX
CC The present sequence is a cDNA encoding farnesyltransferase beta subunit
CC from clone R1R24.pK0007.d6 isolated from rice infected leaf
CC cDNA library R1R24. The present sequence is used in the construction
CC of a chimeric gene to produce transgenic plants with altered level
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC activity may have enhanced tolerance to drought stress. Nucleic acids
CC encoding all or a part of farnesyltransferase proteins can be used in
CC studies to understand cell growth in plants and provide genetic tools to
CC control cell growth and improve tolerance to drought in mature plants.
XX
SQ Sequence 1031 BP; 228 A; 249 C; 302 G; 252 T; 0 other;

```

```

Query Match 4.6%; Score 62; DB 21; Length 1031;
Best Local Similarity 100.0%; Pred No. 8.4e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 820 GGATTTCAAGGACGACAACTAATAATTTGATGCTGCTACTCTTTTGGCAGGAGCT 879
Db 928 GGATTTCAAGGACGACAACTAATAATTTGATGCTGCTACTCTTTTGGCAGGAGCT 987
QY 880 GC 881
Db 988 GC 989

```

Search completed: November 1, 2002, 15:53:15  
Job time : 252 secs

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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:40:44 ; Search time 56 Seconds  
(without alignments)  
5960.999 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359  
Sequence: 1 atggaacccctcccgagtc.....agttcttcgagaagatga 1359

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 38353 seqs, 122816752 residues

Word size : 30

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents\_NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

No matches found

Search completed: November 1, 2002, 17:09:02  
Job time : 56 secs

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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 14:50:49 ; Search time 1797 Seconds  
(without alignments)  
10207.213 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359  
Sequence: 1 atggaccctcccgagtc.....agctcttcagagagtga 1359

Scoring table: OLIGO\_MNC  
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 30

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estinu:\*  
5: em\_estlov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hct:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hct:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inu:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	242	17.8	521	9	BE129712 946003D09
2	232	17.1	533	9	AM120078 614083B05
3	82	6.0	417	9	AM146746 614083B05
4	66	4.9	191	12	AZ916116 Pscl.2.b6
5	32	2.4	582	9	BE194182 HYSME008
6	32	2.4	675	9	AL506683 AL506683
7	32	2.4	715	9	BE214204 HV_CEB000

#### ALIGNMENTS

RESULT 1  
LOCUS BE129712/c 521 bp mRNA linear EST 21-JUN-2000  
DEFINITION 946003D09.XI 946 - tassal primordium prepared by Schmidt Lab Zea  
mays cDNA, mRNA sequence.

ACCESSION BE129712 GI:8577075  
VERSION BE129712.1  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 521)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 946003 row: D column: 09.

FEATURES  
source Location/Qualifiers  
1..521  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="946 - tassal primordium prepared by Schmidt Lab"  
/issue\_type="tassels"  
/dev\_stage="just after the transition from vegetative to inflorescence development"  
/lab\_host="X10LR"  
/note="Organ: tassels; Vector: HybridZAP, Site\_1: EcoRI; Site\_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

BASE COUNT 151 a 118 c 97 g 155 t  
ORIGIN

Query Match 17.8%; Score 242; DB 9; Length 521;  
Best Local Similarity 100.0%; Pred. No. 1.2e-115;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1118	CTCAGTACTAGAGGAGGCTTGAGGATAGCCCTGGAAGACAGAGATCACTATCATT	1177
DB	371	CTCAGTACTAGAGGAGGCTTGAGGATAGCCCTGGAAGACAGAGATCACTATCATT	312
QY	1178	CATGCTACTGCTCAGTACGCTGCGCATGACAGTACGATGATGATGTT	1237
DB	311	CATGCTACTGCTCAGTACGCTGCGCATGACAGTACGATGATGATGTT	252
QY	1238	CGTGCCATTACCTCAGCATGCTTGACCGTACTAATTTGCTGAGCAATCCATC	1297
DB	251	CGTGCCATTACCTCAGCATGCTTGACCGTACTAATTTGCTGAGCAATCCATC	192
QY	1298	CACCTCAATGTTGCTGATAGTACCATACAGCCTATGATTTCTTCAGAAAGT	1357
DB	191	CACCTCAATGTTGCTGATAGTACCATACAGCCTATGATTTCTTCAGAAAGT	132
QY	1358	GA 1359	
DB	131	GA 130	

RESULT 2  
LOCUS AM120078 533 bp mRNA linear EST 22-OCT-1999  
DEFINITION 614083B05.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,  
mRNA sequence.  
ACCESSION AM120078  
VERSION AM120078.1 GI:6095411  
KEYWORDS EST.

SOURCE Zea mays.  
ORGANISM Zea mays.  
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 533)  
AUTHORS Walbot, V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
UNIVERSITY  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614083 row: B column: 05.

FEATURES  
SOURCE  
1. 533  
/organism="Zea mays"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
/clone\_lib="614 - root cDNA library from Walbot Lab"  
/issue\_type="root"  
/dev\_stage="3-4 days old"  
/lab\_host="XLOLR"  
/note="Organ: root; Vector: pBluescriptII SK+; Site: 1;  
EcoRI; Site: 2; XhoI; 3-4 days old root tissue from Walbot  
Lab (LM)"

BASE COUNT 157 a 109 c 103 g 162 t 2 others

ORIGIN  
Query Match 17.1%; Score 232; DB 9; Length 533;  
Best Local Similarity 100.0%; Pred. No. 2.1e-110;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1118 CTCAGTACTAGAGGAGGCTTGAGGATAGCTCGAAGACAGAGATCATCATTT 1177  
|||||  
Db 302 CTCAGTACTAGAGGAGGCTTGAGGATAGCTCGAAGACAGAGATCATCATTT 361  
|||||  
OY 1178 CATGCTACTGCGCTCAGTGGCCTTCAGTACAGCAGTACAGTACGATCATGCTT 1237  
|||||  
Db 362 CATGCTACTGCGCTCAGTGGCCTTCAGTACAGCAGTACAGTACGATCATGCTT 421  
|||||  
OY 1238 CGTCCCATTAAGTACAGATGCTTGGACCGTACTAATTTGCTGAGCCATCATC 1297  
|||||  
Db 422 CGTCCCATTAAGTACAGATGCTTGGACCGTACTAATTTGCTGAGCCATCATC 481  
|||||  
OY 1298 CACTCTACAAATGTTGCTCTAGATAGTACCATACAGCCTATGATCTTCTTC 1349  
|||||  
Db 482 CACTCTACAAATGTTGCTCTAGATAGTACCATACAGCCTATGATCTTCTTC 533  
|||||

RESULT 3  
AM146746 417 bp mRNA linear . EST 03-NOV-1999  
LOCUS AM146746  
DEFINITION 614083B05.y2 614 - root cDNA library from Walbot Lab Zea mays cDNA,  
mRNA sequence.  
ACCESSION AM146746  
VERSION AM146746.1 GI:6194642  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 417)  
REFERENCE Walbot, V.  
AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford  
UNIVERSITY  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V

Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614083 row: B column: 05.  
location/Qualifiers  
1. 417  
/organism="Zea mays"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
/clone\_lib="614 - root cDNA library from Walbot Lab"  
/issue\_type="root"  
/dev\_stage="3-4 days old"  
/lab\_host="XLOLR"  
/note="Organ: root; Vector: pBluescriptII SK+; Site: 1;  
EcoRI; Site: 2; XhoI; 3-4 days old root tissue from Walbot  
Lab (LM)"

BASE COUNT 131 a 79 c 79 g 128 t

ORIGIN  
Query Match 6.0%; Score 82; DB 9; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.2e-31;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1118 CTCAGTACTAGAGGAGGCTTGAGGATAGCTCGAAGACAGAGATCATCATTT 1177  
|||||  
Db 336 CTCAGTACTAGAGGAGGCTTGAGGATAGCTCGAAGACAGAGATCATCATTT 395  
|||||  
OY 1178 CATGCTACTGCGCTCAGTGGCCT 1199  
|||||  
Db 396 CATGCTACTGCGCTCAGTGGCCT 417  
|||||

RESULT 4  
A2916116/c 191 bp DNA linear GSS 15-MAR-2001  
LOCUS A2916116  
DEFINITION Ps1.2\_h6-c-1.0 Maize Ps1 B73 Leaf Zea mays genomic, DNA sequence.  
ACCESSION A2916116  
VERSION A2916116.1 GI:13347388  
KEYWORDS GSS.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 191)  
REFERENCE Missouri Maize Project--Maize Mapping Project.  
AUTHORS Ps1 Zea mays B73 Ps1 Leaf tissue library  
TITLE Unpublished (2001)  
JOURNAL Missouri Maize Project--Maize Mapping Project  
COMMENT Contact: Schroeder S  
Missouri Maize Project--Maize Mapping Project  
University of Missouri  
209 Curtis Hall, Columbia, MO 65211, USA  
Tel: 573 882 8214  
Fax: 573 884 7850  
Email: sschroeder@cecelaphals.agron.missouri.edu  
Class: shotgun.

FEATURES  
SOURCE  
1. 191  
/organism="Zea mays"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="Maize Ps1 B73 Leaf"  
/issue\_type="Leaf"  
/lab\_host="DH5 alpha"  
/note="Organ: Leaf; Vector: pUC19; Ps1 digested B73  
genomic sucrose gradient size fractionated fragment sizes  
of 0.5kb to 2kb ligated to pUC19 transformed in DH5 alpha"  
81 a 36 c 27 g 47 t



Query Match 4.9%; Score 66; DB 12; Length 191;  
Best Local Similarity 100.0%; Pred. No. 2.4e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 591 GGTTCACGACCTTGATATCTTGATTTTAACGCAAAAGGTGTAGCGACATACAT 650  
|||||  
DB 162 GGTTCACGACCTTGATATCTTGATTTTAACGCAAAAGGTGTAGCGACATACAT 103  
|||||

OY 651 AGCAG 656  
|||||

Db 102 AGCAG 97

RESULT 5  
BE194182 582 bp mRNA linear EST 22-OCT-2001  
LOCUS HVSMEH0084H13f Hordeum vulgare 5-45 DAP spike EST library  
DEFINITION HVCNMA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0084H13f,  
mRNA sequence.  
ACCESSION BE194182  
VERSION BE194182.1 GI:8706368  
KEYWORDS EST.  
SOURCE barley.  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Hordeum.  
1 (bases 1 to 582)  
Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu  
,X., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton  
,R.D., Close,S.J., Oates,R. and Main,D.  
Development of a genetically and physically anchored EST resource  
for barley genomics: Morex 5-45 DAP spike cDNA library  
Unpublished (2001)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total hg bases = 161  
Seq primer: AATTACCTCTCAGTAAGCG  
High quality sequence start: 12  
High quality sequence stop: 527.  
Location/Qualifiers  
1..582  
/organism="Hordeum vulgare"  
/cultivar="Morex"  
/db\_xref="taxon:4513"  
/clone="HVSMEH0084H13f"  
/clone\_1lb="Hordeum vulgare 5-45 DAP spike EST library  
HVCNMA0009 (5 to 45 DAP)"  
/tissue\_type="5-45 DAP Spike"  
/lab\_host="SOLR"  
/note="Vector: lambdaZAP. Site\_1: EcoRI; Site\_2: XhoI;  
Plants were grown in the greenhouse at the University of  
California, Riverside (Fenton, SJ Close, TJ Close). Whole  
spikes with awns trimmed were collected at 5, 10, 15, 20,  
30 and 45 DAP (Fenton). Total RNA was prepared from each  
pool, equal quantities of all six RNA pools were combined,  
poly(A) RNA was purified from the mixture, one primary  
unamplified cDNA library was made, and 1 million pfu were  
in vivo excised to give plasmid SK(-) cDNA phagemids  
(Choi) in the TJ Close lab at the University of California,  
Riverside. Phagemids were plated and picked at the Clemson  
University Genomics Institute (CUGI) (Begum, Palmer,  
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
sequencing and sequence analysis were performed at CUGI  
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
The sequence has been trimmed to remove vector sequence  
and contains a minimum of 100 bases of phred value 20 or  
above. For more details on library preparation and

sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
this clone see <http://www.genome.clemson.edu/orders> Also  
see Close TJ, Wing R, Kleinof A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30  
(<http://wheat.pw.usda.gov/ggpages/dgn/31/cover.html>)"

BASE COUNT 123 a 168 c 176 g 114 t 1 others

ORIGIN

Query Match 2.4%; Score 32; DB 9; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GTGACGACGTGAGCAGATGAGTGAGGC 113  
|||||  
DB 171 GTGACGACGTGAGCAGATGAGTGAGGC 202  
|||||

RESULT 6  
AL506683 675 bp mRNA linear EST 04-JUN-2001  
LOCUS AL506683  
DEFINITION Hordeum vulgare Barke developing caryopsis (3..15.DAP)  
Hordeum vulgare cDNA clone HY03022T 5', mRNA sequence.  
ACCESSION AL506683  
VERSION AL506683.1 GI:12032898  
KEYWORDS EST.  
SOURCE barley.  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Hordeum.  
1 (bases 1 to 675)  
Michalek,W., Wesccke,W., Pleissner,K.-P. and Graner,A.  
EST sequencing and analysis in barley  
Unpublished (2000)  
Contact: Michalek W  
Institute for Plant Genetics and Crop Plant Research  
Corrensstr.3, D-06466 Gatersleben, Germany  
Email: michalek@ipk-gatersleben.de, <http://pgrc.ipk-gatersleben.de>  
Seq primer: T3 primer for 5'end.  
Location/Qualifiers  
1..675  
/organism="Hordeum vulgare"  
/cultivar="Barke"  
/db\_xref="taxon:4513"  
/clone="HY03022T"  
/clone\_1lb="Hordeum vulgare Barke developing caryopsis  
(3..15.DAP)"  
/tissue\_type="developing caryopsis (3..15.DAP)"  
/lab\_host="XLOLR"  
/note="Vector: plasmid pRK-CMV. Site\_1: EcoRI; Site\_2:  
XhoI. mRNA was made from developing caryopsis (3..15.DAP)  
of spring barley variety 'Barke', a high quality malting  
variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI  
(3'-end of cDNA). NOTE: Due to a cloning artefact caused  
by the kit, in most cases the EcoRI site is NOT present,  
as well as the EcoRI adapter. Average insert size is 1 kb  
Sequence trimming: Vector sequences and sequence ends were  
trimmed from the 5'- and 3'-end until a 50 bp window  
contains less than two ambiguities. The maximum length was  
set to 700 bp"

BASE COUNT 149 a 185 c 199 g 138 t 4 others

ORIGIN

Query Match 2.4%; Score 32; DB 9; Length 675;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GTGACGACGTGAGCAGATGAGTGAGGC 113  
|||||  
DB 191 GTGACGACGTGAGCAGATGAGTGAGGC 222  
|||||

RESULT 7  
BE214204  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

BE214204 715 bp mRNA linear EST 23-OCT-2001  
HV\_CEB0002K12f Hordeum vulgare seedling green leaf EST library  
HVCNDA0005 (Blumeria challenged) Hordeum vulgare cDNA clone  
HV\_CEB0002K12f, mRNA sequence.  
BE214204  
BE214204.3 GI:16335375  
EST.  
SOURCE  
Hordeum vulgare  
barley.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Hordeum.  
1 (bases 1 to 715)  
Wing, R., Close, T.J., Kleinholz, A., Wise, R., Wei, F., Begum, D.,  
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi,  
D.W., Fenton, R.D., Oates, R. and Main, D.  
Development of a genetically and physically anchored EST resource  
for barley genomics: Blumeria infected incompatible (Mia6) seedling  
leaf cDNA library  
Unpublished (2001)  
On Jul 3, 2000 this sequence version replaced gi:13263971.  
Contact: Wing, R.A.  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total hg bases = 422  
Seq primer: AATTAACTCTCACTAAAGCG  
High quality sequence stop: 555.  
Location/Qualifiers  
1..715  
/organism="Hordeum vulgare"  
/cultivar="C16151 (Mia6)"  
/db\_xref="taxon:4513"  
/clone\_lib="HV\_CEB0002K12f"  
/clone="HV\_CEB0002K12f"  
/library="HVCNDA0005 (Blumeria challenged)"  
/tissue\_type="seedling green leaf"  
/lab\_host="SOLR"  
/note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI;  
C.I. 16151 (Mia6) plants were greenhouse grown in the R  
Wise lab at Iowa State University, Ames, IA; 7 day old  
green seedlings were challenged with isolate 5874 (AvrMia6  
) of Blumeria graminis f. sp. hordei, and leaves were  
harvested 20 and 24 hr post-inoculation and snap frozen;  
uninoculated leaves were harvested 20 hr post-inoculation  
(Wei, Wise). In the T3 Close lab at the University of  
California, Riverside, total RNA was prepared from each  
sample pool, equal quantities of all three RNA pools were  
combined, poly(A) RNA was purified from the mixture, one  
primary unamplified cDNA library was made, and 1 million  
pfu were in vivo excised to give plasmidscript SK(-) cDNA  
phagemids (Choi, Close). Phagemids were plated and picked  
at the Clemson University Genomics Institute (CUGI) (Begum  
, Palmer, Frisch, Atkins and Wing). Plasmid DNA  
preparations, DNA sequencing and sequence analysis were  
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates  
, Rambo, Main). The sequence has been trimmed to remove  
vector sequence and contains a minimum of 100 bases of  
phred value 20 or above. For more details on library  
preparation and sequence analysis see  
http://www.genome.clemson.edu/projects/barley. To order  
this clone see http://www.genome.clemson.edu/orders Also  
see Close T.J., Wing R., Kleinholz A., Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30.  
(http://wheat.pw.usda.gov/g9pages/ug9n/31/cover.html)"

BASE COUNT  
162 a 189 c 219 g 145 t

ORIGIN  
Query Match 2.4%; Score 32; DB 9; Length 715;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 82 GTGACCGAGGTGAGCAGATGAAGGTGAGGC 113  
DB 172 GTGACCGAGGTGAGCAGATGAAGGTGAGGC 203  
Search completed: November 1, 2002, 16:23:28  
Job time : 1799 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 12:41:24 ; Search time 2651 Seconds  
(without alignments)  
10727.712 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359  
Sequence: 1 atgagaccctcccgagtc.....agttctctcagaagatga 1359

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_ln:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ov:\*  
8: gb\_ov:\*  
9: gb\_ov:\*  
10: gb\_ov:\*  
11: gb\_ov:\*  
12: gb\_ov:\*  
13: gb\_ov:\*  
14: gb\_ov:\*  
15: gb\_ov:\*  
16: gb\_ov:\*  
17: gb\_ov:\*  
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19: gb\_ov:\*  
20: gb\_ov:\*  
21: gb\_ov:\*  
22: gb\_ov:\*  
23: gb\_ov:\*  
24: gb\_ov:\*  
25: gb\_ov:\*  
26: gb\_ov:\*  
27: gb\_ov:\*  
28: gb\_ov:\*  
29: gb\_ov:\*  
30: gb\_ov:\*  
31: gb\_ov:\*  
32: gb\_ov:\*  
33: gb\_ov:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query Match Length DB ID Description

1	452.2	33.3	1449	8	NGU73203	U73203 Nicotiana g
2	452.2	33.3	1832	8	LE083708	U83708 Lycopersico
3	449.4	33.1	1648	8	PEABFARNES	L08664 Pea farnesy
4	424.8	31.3	1627	8	AF214106	AF214106 Arabidops
5	402	29.6	1331	8	ATU44849	U44849 Arabidops
6	206.6	15.2	2464	6	AR077271	AR077271 Sequence
7	206.6	15.2	2464	6	AR102373	AR102373 Sequence
8	206.6	15.2	2464	6	AR102373	AR102373 Sequence
9	206.6	15.2	2464	6	AR102373	AR102373 Sequence
10	203.6	15.0	1413	6	RATFRTS	M69056 Rat farnesy
11	202	14.9	1314	6	AR048524	AR048524 Sequence
12	202	14.9	1314	6	AR048524	AR048524 Sequence
13	202	14.9	1314	6	AR048524	AR048524 Sequence
14	200.4	14.7	1248	6	AR077273	AR077273 Sequence
15	200.4	14.7	1248	6	AR077273	AR077273 Sequence
16	200.4	14.7	1248	6	AR077273	AR077273 Sequence
17	199.2	14.7	1314	6	AR048522	AR048522 Sequence
18	199.2	14.7	1314	6	AR048522	AR048522 Sequence
19	197.2	14.5	2546	6	AR048523	AR048523 Sequence
20	179.6	13.2	86743	3	AP003218	AP003218 Oryza sat
21	161	11.8	40961	3	CBRG27D19	AC084541 Caenorhab
22	153.6	11.3	1588	3	AY051869	AY051869 Drosophill
23	144	10.6	34882	2	AC014444	AC014444 Drosophill
24	144	10.6	199653	3	AC011615	AC011615 Drosophill
25	144	10.6	225795	3	AE003713	AE003713 Drosophill
26	112.2	8.3	27797	3	CE23812	CE23812 Drosophill
27	110	8.1	63923	2	AC008292	AC008292 Drosophill
28	87.4	6.4	43880	8	SPAC17G6	M22753 S. pombe chr
29	83.4	6.1	1958	8	YSCDPR	M22753 S. pombe chr
30	83.4	6.1	2060	8	SCYDL090C	Z74138 S. cerevisia
31	83.4	6.1	38516	8	SCCHRIVLA	X95644 S. cerevisia
32	81	6.0	13066	8	U75644	X95644 S. cerevisia
33	78.2	5.8	3174	8	ABU46574	U46574 Arabidops
34	78.2	5.8	61001	8	ABU10699	ABU10699 Arabidops
35	59.2	4.4	1758	3	AF230369	AF230369 Trypanoso
36	59	4.3	1306	6	AR123105	AR123105 Sequence
37	59	4.3	1306	6	AR123105	AR123105 Sequence
38	56	4.0	1138	9	HSU49245	U49245 Human geran
39	54.6	4.0	154499	2	AC096084	AC096084 Rattus no
40	54.4	4.0	1179	9	HSGG11	X98001 H. sapiens m
41	54.4	4.0	1526	9	BC020790	BC020790 Homo sapl
42	52.8	3.9	1374	9	HSRABCRB	Y08201 Homo saplen
43	51.6	3.8	69622	2	AC101674	AC101674 Mus muscu
44	51.4	3.8	190517	9	CNS01DX4	AL190222 Human chr
45	49.2	3.6	1230	6	AR123106	AR123106 Sequence

## ALIGNMENTS

RESULT 1  
LOCUS NGU73203 1449 bp mRNA linear PLN 17-DEC-1996  
DEFINITION Nicotiana glutinosa farnesyltransferase beta subunit mRNA, partial cds  
ACCESSION U73203  
VERSION U73203.1 GI:1732586  
KEYWORDS  
SOURCE  
ORGANISM Nicotiana glutinosa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
REFERENCE  
AUTHORS Zhou, D., Yang, Z., and Cramer, C.L.  
TITLE A cDNA Clone Encoding the beta Subunit of Protein Farnesyltransferase from Nicotiana glutinosa (accession No. U73203) (PGR96-109)  
JOURNAL Plant Physiol. 112, 1398 (1996)  
REFERENCE  
AUTHORS Zhou, D., Yang, Z., and Cramer, C.L.  
TITLE Direct Subunit  
JOURNAL Submitted (02-OCT-1996) Plant Pathology, Physiology and Weed



FEATURES California Berkeley, 111 Koshland Hall, Berkeley, CA 94720, USA  
source Location/Qualifiers  
1.1832  
/organism="Lycopersicon esculentum"  
/cultivar="WFN Cherry LA1221"  
/db\_xref="taxon:4081"  
1.1832  
/gene="LeftB"  
69.1481  
/gene="LeftB"  
/note="similar to Saccharomyces cerevisiae Ramlp"  
/codon\_start=1  
/product="farnesyl protein transferase subunit B"  
/protein\_id="AAC49666.1"  
/db\_xref="GI:1815668"  
/translation="MESRYVTKLEDDWVERREIVDYFYSISPSPDLIEIRD  
KHEGYLSQGRKJGFSEVYLDARPMICWTLISLISGKSPNDLIDLTGCO  
DKDGGGGGPGMPLATYAAVNSLITGKPAISINERKYLTLRMRKSGGPR  
MHGGEVDRACITAIISVNIILTYDELHIGYNTLSQTEGGIAGEBSEAHG  
YFEGLAAILINEVDRLDPLIDWVEREVEGFGQRTNLLVDCYSFWGAVF  
LIORNLIVHEDDGLSNDLSTESADSSSELDEBHEGLSSHVDFTPLGAGAC  
QENASHSPKIDYGEFINKPIAMRPLFDSMYLQOYVLLCSQIEVGGFRDKPKGGRDY  
YHTCYLSGISLISYMTDEADSTPLPRDYFGPYSKLLQVHPLFNVLDRIYEARE  
YSGCFEVSPLSLAPFSEF"

BASIS COUNT 530 a 328 c 426 g 548 t  
ORIGIN

Query Match 33.3%; Score 452.2; DB 8; Length 1832;  
Best Local Similarity 60.8%; Pred. No. 6.5e-109;  
Matches 816; Conservative 0; Mismatches 458; Indels 69; Gaps 2;

72 GAGGCTCAGGTCAGCAGGTGAGCAGATGAGGTGAGGCCAGGTTGGCAGCATCTA 131  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
80 GAAAGTGACGAGACCGCTGGAAGATCAATGGTGTGAGCGTCGAGTCGAGATATA 139  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
132 CCGCTCCCTCTTGGGGGCCGCCACAGCAATCCATCATCTAGAGCTGTGGCTGA 191  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
140 CGATTATTTCTACAGCACTTCCGCCAACCTCCGTCGACCTCAVGAAGATCGAGTGA 199  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
192 TCAGCATATCGAGTATCTGACGCTGGCTGAGCATATGGAGCAGCCCTTCATGTTCT 251  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
200 CAACACTCTGGGTATCTAAGCCAAAGCTCAGAAAACCTGGCTGCTTCCGTTT 259  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
252 AGATGCCAATCGCCCTGGCTATCTGATGATGATTCATCCACTCTTGTCTGATGA 311  
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
260 GGATGCCAGTCGACCAAGCTTGTCTACTGACACTTCATTCATCCCTTGTGGGAGA 319  
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
312 AGCACTGATGATGATCTGGAATGATATCATGACTTCTTACTGATGATGCGATTA 371  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
320 ATCTATTGTGGCAACTGGAAATGATGCAATGACTTCTGACCCGTCGCGATTA 379  
11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
372 AGATGTGATATAGTGTGACCTGAGACAGTTGCTCACCTAGCTACGACTTATGCTGC 431  
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
380 AGATGTGCTATGAGAGTGTGACCTGCTCAGATGCCCTCATCTTGCACACTACTTATGCTGC 439  
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
432 TGTAAATACACTTGTGCAATAGGAGCGAAAGAGACTGTTCATCAATCAATAGGCGCA 491  
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440 AGTCAATTAATTAATTAATTTGGGCAAACTGAAAGCTCTGTGTCATCAATTAATAGAA 499  
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492 CCGTCAATTTATGCTGCAAGATGAAAGATGTATCAGGTGCTTTCAGATGATGATG 551  
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500 GTTGTACACATTTTGTGCAAGAAAGAGCGAAGTGTGATTCAGATGCGCATGCG 559  
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552 TGGCAATATGATGTCCGCTTCTACACCGCTATTCGTTGCCGCCCTTGGATAT 611  
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560 TGGAGAAATGATGTGTGCTGCTTATTAATGCAATTTCTGTTGCAATTAATTAATCAT 619  
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612 TCTGATTTTAACTGCAAAAGGTGTAGCGACTACATAGCAAGATGCTCAAACTTATGA 671  
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620 TGTGATGAGCAGAGCTGATGTGTGGAATTAATTAATCAAGTCTCAGACTTATGA 679  
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672 AGGTGATTTGCTGGGAGCCTTATGCTGAAGCAGCATGTTGGGTATTAATTTCTGATTT 731  
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Db 680 AGGTGAATTTGCTGGCGCAACCGGTTCTGAAGCTCATGTTGGGTATCTTCTGTGGCTT 739  
732 GAGCTCTTTGATCTGCTGCTTAATGAGCAGAAAGTGTGACTTGGCTAGTTGATTTGGCTG 791  
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Db 740 GCGTGCATATGATTTGATCAACGAAAGTATGATCGATTGGACTTGGCAGCTTAAATTTGATTG 799  
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Qy 792 GGTGGCTTTTTCGTCAGAGAGTGAATGCGATTTTCAAGAGCAACTAATAATTTGTTGA 851  
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Db 800 GTGTGATTTAGCAAGAGGGTGCAGAGGTGATTTCAAGCGCAGCAATATAATTAATGTCGA 859  
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Qy 852 TGTGTGCTACTCCCTTTTGGCAGAGAGCTGCCATTCCTTTACACAAAAGTTAATTAAGAT 911  
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Db 860 TGTGTGATTTCTTTTGGCAGAGGGCGGTAGTGTTCCTTAATCAAGAACTAATTTGAT 919  
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Qy 912 TGTGATTAAGCAATTTGAAGTCCCTGATTCCTGCAAAAAGCCATCAGAGAGATGCTGCTG 971  
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Db 920 AGTCAATGAACCACTAGGGCTGTCAATTAATGACCTAGTAACAGAAAGTCTGATTTCTTC 979  
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Qy 972 CAGCAGCAATTCATATGGGTGCACCGCA----- 1000  
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Qy 1001 -----AAAAGTCTCCCTGCTGTGGACTA 1025  
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Db 1040 TACTTCCCTCTTGGACAAGCAGTCTGTTCAAGAAAATGCTTCTCATAGCCCAAAAT 1099  
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Qy 1026 TGGCAAGTTTGGATTTGATTTATATACAAGAGCAGCAACCAATTTGGCCACTCTTCATTA 1085  
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Db 1100 AGCAGATATCTGATATGATTTATCAACGCCATATGCTATGAGGCTCTCTTTGACAG 1159  
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Qy 1086 CATTTGCCCTGCAACATATCATCTTCTTGTCTGAGGTACTAGAGGAGGCTTGGAGGA 1145  
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Db 1220 CAACCTGGGAGAGGTGAGACTACTACATCCCTGTTAGTTAAGTGTCTTTCAAT 1279  
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Qy 1206 TAGCAGTACAGTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1265  
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Db 1280 TGCTAGATATGCTGAGCAGCAGAGGTGATTAACACATATCCAGAGGATGATTTGG 1339  
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Qy 1266 ACCGTACTTAA---TTGCTGGAGCCATGATGATGATGATGATGATGATGATGATGAT 1332  
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Db 1340 TCCATTATTCAAATGCTGTTGGAAAGGTTACCCACTTCAAGAGTGTGATGATG 1399  
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Qy 1323 GTACCATAGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1345  
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Db 1400 GTATTATGAGCTGCGGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1422  
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RESULT 3  
PEARFARNES 1648 bp mRNA linear PLN 14-JUL-1993  
LOCUS PEARFARNES 1648 bp mRNA linear PLN 14-JUL-1993  
DEFINITION Pea farnesyltransferase beta-subunit mRNA, complete cds.  
ACCESSION 108664  
VERSION 108664.1 GI:169048  
KEYWORDS beta-subunit; farnesyltransferase.  
SOURCE Pison sativum (Library: Clontech) seedling apical bud cDNA to mRNA.  
ORGANISM Pison sativum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;  
Pisum.  
REFERENCE 1 (bases 1 to 1648)  
AUTHORS Yang,Z., Cramer,C.L. and Watson,J.C.  
TITLE Protein farnesyltransferase in plants. Molecular cloning and  
expression of a homolog of the beta-subunit from the garden pea  
JOURNAL Plant Physiol. 101, 667-674 (1993)  
MEDLINE 94105305  
FEATURES Location/Qualifiers  
1.1648  
/organism="Pison sativum"

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ORIGIN					

Query Match	33.18;	Score 449.4;	DB 8;	Length 1648;
Best Local Similarity	63.78;	Pred. NO. 3.5e-108;		
Matches 731;	Conservative 0;	Mismatches 386;	Indels 30;	Gaps 2;

QY	243	TCATTTTCTAGATGCCAATCGCCCTGGCTAGTCACTAGCAAGTGTTCATCCACTGGCTT	302
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QY	303	GCTGCATGAAGCACCTTGTATGATGATCTTGGAGATCATATCAGACTCTTACGTCGATG	362
Dp	258	GTTGGGAACATCTAATGTATGATGATCTCGAAGATTAACCTGTGCATTTTCTTAAACCGTTG	317
QY	363	TCAGATTAAGATGGTGGATATAGTGTGGAGACCTCGACAGTGGCCCTCACTAGTCAACGC	422
Dp	318	CCAGATATCCAAATGGTGGATATGCTGGGGAGACCTGTGCATATGCTCATCTTTGCCACATC	377
QY	423	TTATGCTCTGTAAATACACTTGTGACAAATAGGAGCGAAGAGCATTTCTCATCAATCAA	482
Dp	378	TTATGCTCAGCATACCTACTTATTAACCTGTGGGTGTGAAATCTTTGGCATCTATTAA	437
QY	483	TAGGGGCAACCTGTGCANATTTATCTGTGCAGATGAAAGATGTATACAGTGCTTTACAGAT	542
Dp	438	TAGAATATAAGTTATCGCGTTTATCGCGGGATGTAACACGCCAAACGGGGATTTACGAT	497
QY	543	GCATAGTGGTGGCAAAATTTGATGTCGGTCTCTTCAACCCGTATATCGGTTGCCAGCCT	602
Dp	498	GCATACGAGGGAGAAATTTGACGTTTCGAGCTTGCATCTGCTACACTGGCCATCTGTGTGGCAATGT	557
QY	603	TGTGAATATTCTGATTTTAACTGGCAAAAGGTATAGCGACTACATNACAAATGTCA	662
Dp	558	TCGTGAACATTTTGGATGTATGACCTGATCAAGATCTTGGAGACTTCATTTTAAAGCTGCA	617
QY	663	AACTATTAAGGTGTATTTTCTGGGGAGCCCTATCTGTAAGACATATGGGGTATACATTT	722
Dp	618	AACATATAGGAGGCCCTTGTGCTGTGAGCCCTGGTCTGTAGGCTCATGTGGGGTATACCTTT	677
QY	723	CTGTGCATTTGCCTGTTTGATCTCTCTTAATGAGCGACAGAAAGTTGACTTGGCTAGTTT	782
Dp	678	TTTGTCGTTAGTCGCAATCATCTCATTTGGTATGCTTAATCCCTGGATCTTCCCTGCTTT	737
QY	783	GATTCGCTGGGCGCTTTTTCGTCAAGGAGTGAATGGCGATTTTCAAGGACGACAAATATA	842
Dp	738	ACTTATATTGGGTGTGTCTTTCGGCAAGGTAAGAGTGTGATTTCAAGGGAGCAACAAATTA	797
QY	843	ATTGCTTGAATGTTCTACTCTCTTTTGGCAGGAGCATCCATGCTTTTCACACAAGATTT	902
Dp	798	ATTGCTAGATGATCTACTGCTTTTGGCAGGAGAGTGTCTGTGGCCCTAATTCGCAAGATTT	857
QY	903	AATTACGATTTGTTCAAGCAATTTG-----AACTCCTCGTATTTCTGTGC	945

[illegible]

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AF214106 RESULT 4
LOCUS AF214106 1627 bp mRNA linear PLN 21-JUN-2000
DEFINITION Arabidopsis thaliana farnesyltransferase beta subunit (ERAI) mRNA,
complete cds.
ACCESSION AF214106
VERSION AF214106.1 GI:8347239
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 1627)
AUTHORS Ziegelhofer,E.C., Medrano,L.J. and Meyerowitz,E.M.
TITLE Cloning of the Arabidopsis WIGGUM gene identifies a role for
farnesylation in meristem development
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (13), 7633-7638 (2000)
MEDLINE 20319078
REFERENCE 2 (bases 1 to 1627)
AUTHORS Ziegelhofer,E.C., Medrano,L.J. and Meyerowitz,E.M.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1999) Biology, California Institute of
Technology, 1200 East California Boulevard, Pasadena, CA 91125, USA
FEATURES
Source
location/Qualifiers
1..1627
/organism="Arabidopsis thaliana"
/cultivar="Landsberg erecta"
/db_xref="taxon:3702"
/chromosome="5"
/map="15 kb from top, between tt2 and gl3"
1..1627
/gene="ERAI"
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1..1449
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Query Match 29.6%; Score 402; DB 8; Length 1331;  
Best Local Similarity 60.0%; Pred. No. 1.3e-95;  
Matches 722; Conservative 0; Mismatches 455; Indels 27; Gaps 2;

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QY 178 GAGCTGGCGGTATCGCATATCGAGTATCTGACCGCTGGAGGCAATATGAGCA 237
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DB 1 GACATTCACGCAATGAAATGATATCTGAAAGCGCTTAAAGCGCTTGGCCG 60
QY 238 GCGTTTCATCTTGTAGATGCAATCGCCCTTGGCTATGCTAGTGAATGATTCACCT 297
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DB 61 CAGTTTCTCTCTTGTAGATGCAATCGACCTTGGCTTGTACTGATTCATTCATATA 120
QY 298 GCTTTCGTGATGAAAGCACTTGTATGATCTTGAGAAATGATATCATAGATCTTAACT 357
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DB 121 GCTTTCGTGAGAGACTGTGATGATGAAATGAAAGCAATGCAATGCACTTCTTGA 180
QY 358 CGATGTCAGATTAAGATGCTGATATAGTGTGAGACCTGGACAGTTGCTCAGCTTAC 417
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DB 181 CGCTGCCAGGCTCTGAAAGGTGATAGCGTGTGCTGCGCAACTTCCAGATCTTGA 240
QY 418 ACGACTTATGCTGCTGTAATACACTTGTGACAAATAGAGAGCAAGAGCTTGTATCA 477
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DB 241 ACTACTTATGCTGAGTGAATGCACTTGTACTTTAGAGAGTGAACAAGCCCTTCTTCA 300
QY 478 ATCAATAGGGGCAACTCTGCAATTTTATGCTGAGATGAAGAATGATGAGTGTTC 537
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DB 301 ATTAAATGAGAAAATAATGCTTTTAAAGCGATGAAGATACAACTGAGAGCTTTC 360
QY 538 AGATGATGATGCTGCGCAATTTGATGCTGCTTCCACACCGTATATGCTTGGTCC 597
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DB 361 AGCATGATATATGAGCAAAATTTGATGCTGCTGCTACACTGCAATTTGGTTTGA 420
QY 598 AGCCTGTGATATTTCTGATTTTAACTGCAAAAGGTAGCGCATACATACAGAGA 657
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DB 421 AGCATCTTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 658 TGTCAAACTATGAGTGTATGCTGCGGAGCTTATGCTGAGACACATGCTGCTAT 717
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DB 481 TGCCAACTATGAGTGTATGCTGCGGAGCTTATGCTGCGGAGCTTATGCTGCTAT 540
QY 718 ACATTCGTGATTTGCTGCTTGTGATCTGCTTAAATGAGGAGCAAAAGTTGATGCT 777
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DB 541 ACCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 778 AGTTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
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DB 601 TCATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 838 AATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
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DB 661 AACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 898 AAGTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
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DB 721 AGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 955 TCAAGAGAGA-----TGCTGCAAGCAGCAGCTTGTATGAGG 990
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DB 781 AATGAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 991 TGCACCGCGAAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
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DB 841 TCTGATGAGGACAAAGATGAAATTCAGTGAATGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 1051 CAAGAGAGCAACAAATTTGGCCCACTTTCATTAACATTTGCTGCAACATATACATCTTA 1110
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DB 901 TACATTAACAGAGATGCACTGCTTGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 1111 CTTTGTCTAGGTACTAGAGAGGCTTGGAGATTAAGCTGGAAGAGCAGAGATGAC 1170
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DB 961 TTGTGCTTAAGATCCTGAGGCTGATTCAGAGACAAAGCCGAGAAAGCCGCTGACTTC 1020
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QY 1171 TATCATTCATGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1230
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DB 1021 TACCAACATGTTAGTACGCTGAGGAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1231 ACTGCTTCTGCTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1290
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DB 1081 GAGGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1291 ATCCATTCACCTTACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
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RESULT 6  
AR077271  
LOCUS AR077271 2464 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 4 from patent US 5962243.  
ACCESSION AR077271  
VERSION AR077271.1 GI:10004017  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 2464)  
AUTHORS Brown,M.S., Goldstein,J.L. and James,G.L.  
TITLE Methods for the identification of farnesyltransferase inhibitors  
JOURNAL Patent: US 5962243-A 4 05-OCT-1999;  
FEATURES  
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/organism="unknown"

BASE COUNT 556 a 705 c 630 g 573 t  
ORIGIN

Query Match 15.2%; Score 206.6; DB 6; Length 2464;  
Best Local Similarity 56.7%; Pred. No. 1.1e-43;  
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

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QY 172 ATCTGAGCTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 231
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DB 267 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
QY 232 GGACACGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
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DB 327 ACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
QY 292 CCACCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
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DB 387 AGCTTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446
QY 352 TTGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
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DB 447 TTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
QY 412 CTAGCTAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
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DB 507 CTGCTGCCAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
QY 472 TCATCATCAATGAGGCAACTGTACAAATTTTATGCTGCTGCTGCTGCTGCTGCTGCT 531
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DB 567 AACGTATTAACAGAGAGAGAGCTCTTACGATCTTACTTCTTAAAGCAACCGATGCTG 626
QY 532 GCTTTCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
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DB 627 TCTTTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686
QY 592 GTTGCACGCTTGTGATATTTCTGATTTTAACTGCAAAAGGCTTAGCGCCTACATATA 651
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DB 687 GTAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
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QY	652	GCACGATCTCAACCTTATGAAAGCGTGTATTTGCTGGGAGCCCTTATGCTGAAACACATGCT	711
Db	747	GCAAGTCCCAAGAACTGGGAAGCCGGCAATTGGCGSSGGGTCCACAGGATGSAAGCCCAAGCT	806
QY	712	GAGATATACATCTCTGTGATTTGGCTGCTTTGATCTGCTTAATGAGGACGAGAAAGTTGAC	771
Db	807	GAGCTACACCTTCTGTGGCTTGGCTCGCTGGATCTCAACAGAAAGCACTTCTTTGAGC	866
QY	772	TTGCCTACTTTGATTGGCTGGGTGGCTTTTCTCA---AGAGGTGGAAATCCGGAATTTTCAA	828
Db	867	CTGAAGACCTTGCTCAACAATGGGTGACAAGCCGGCAGATGCGGTTTCAAGAGAGGATTTTCAG	926
QY	829	GGACGAACTAATTAATTTGGTTGATGGTTGCTACTCTTTTGGCAGGAGG	877
Db	927	GGCCCTCTCAACAACGCTGCTGACGGCTGCTACTCTTCTGTGGCAGGACG	975

RESULT	7			
ARI02373				
LOCUS	ARI02373	2464 bp	DNA	linear
DEFINITION	Sequence 4 from patent US 6083917.			
ACCESSION	ARI02373			
VERSION	ARI02373.1	GI:12813171		
KEYWORDS				
SOURCE	Unknown.			

REFERENCE 1 (bases 1 to 2464)  
AUTHORS Brown,M.S., Goldstein,J.L., Reiss,Y. and Marsters,J.  
TITLE Methods and compositions for the identification, characterization  
and inhibition of farnesyltransferase  
JOURNAL Patent: US 6083917-A 4 04-JUL-2000;  
FEATURES Location/Qualifiers  
source 1. 2464

BASE COUNT	556 a	705 c	630 g	573 t
ORIGIN				

Query Match	15.28	Score	206.6	DB	6	Length	2464
Best Local Similarity	56.78	Pred. No.	1,1e-43				
Matches	402	Conservative	0	Mismatches	304	Indels	3
						Gaps	1

[illegible]

QY	652	GCAGATGTCAAACCTTAAGAAAGTGGTATTCCTGGGAGACCTTAATGCTGAAGACACATGGT	711
Db	747	GCAGATGCCCAAGAACTGGGAAAGCCGGCAATTGGCGGGGTGCCAGGATGGAAGCCACAGCT	806
QY	712	GGGTAATACATTCCTGATGATTGGCTGCTTTGATCCTGCTTAATGAGCGAGAAAGTTGAC	771
Db	807	GGCTACACCTTCTGTGGCTTGGCTCGCTGGTGAATCCTCAAGAAAGAAAGCTTCCTTTCAC	866
QY	772	TTTGCTATTTCATGATGGCTGGGTGGCTTTTGCTCA --- AGCAGTCGATGCGGATTTCAA	828
Db	867	CTGAAGACCTTGGCTACAAATGGGTGACAAAGCCGGCGAGATCCGCTTCGAAGAGGAGATTTCA	926
QY	829	GGAGCAACCTAAATTAATTTGGTTGATGGTTGCTACTACTCTTTGGCAGAGGAC	877
Db	927	GGCCCCCTCAACAAAGCTGGTGAAGCGCTGCTACTACTCTTCTGGCAGAGGAC	975

RESULT 8			
LOCUS	112220		
DEFINITION	Sequence 4 from patent US 5420245.	2464 bp	DNA
ACCESSION	112220		Linear
VERSION	112220.1	GI:909718	PAT 26-JUL-1995
KEYWORDS	.		

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REFERENCE 1 (bases 1 to 2466)
AUTHORS Brown,M.S., Goldstein,J.L. and Reiss,Y.
TITLE Tetrapeptide-based inhibitors of farnesyl transferase
JOURNAL Patent: US 5420245-A 4 30-MAY-1995;
FEATURES Location/Qualifiers
SOURCE 1. 2464
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BASE COUNT	556 a	705 c	630 g	573 t
ORIGIN	/organism="unknown"			

Query Match	15.2%	Score 206.6	DB 6	Length 2464
Best Local Similarity	56.7%	Pred. NO. 1.1e-43		
Matches 402	Conservative 0	Mismatches 304	Indels 3	Gaps 1

[illegible]

	QY	652	GCAACATCTCAAACCTTATTGAAGAGCGTGTTATGCTGGGGAGCCCTTATTCGTGAACCATCATGCT	711
	Db	747	GCMAGCTGCCAAGACTGGGAMGCGGCATATGGCGGGGTGCCAGGAGTAGAACCCACGCT	806
	QY	712	GCGATTACATCTCTGTGATTGGCTCCTTTGATCCTGCTTAATGAGCGACAAGAAGTTGAC	771
	Db	807	GGCTACACCTTCTCTGGCTTGCGCTCGCGTGGTGATCTCAACAGAAAGACCTTCTTGAAC	866
	QY	772	TTCGCTACTTTGATTTGCGCTGGGTGGCTTTTGTCTCA---AGACGTGATCCGGAATTTCAA	828
	Db	867	CTGAAGACCTTGCTCAACATGGGTGACAAGCCGGCAGATCCGGTTGCAAGAGGAAATTTGAG	926
	QY	829	GGACGAACTTAATAATTGGTTGATGATTGCTACTCCTTTTGGCAGAGGAG	877
	Db	927	GGCGCCCTGCACAAACACTGTGTGAGCGGCTGCTACTCTTGSCAGACGAG	975
	RESULT 9			
	RATFBS			
	DEFINITION	Rat farnesyltransferase beta subunit mRNA, complete cds.	2464 bp	linear ROD 27-APR-1993
	ACCESSION	M69056		
	VERSION	M69056.1 GI:204185		
	KEYWORDS	farnesyltransferase.		
	SOURCE	Rattus norvegicus (strain Sprague-Dawley) brain cDNA to mRNA.		
	ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	REFERENCE	1 (bases 1 to 2464) Chen,W.-J., Andres,D.A., Goldstein,J.L., Russell,D.W. and Brown,M.S. cDNA cloning and expression of the peptide-binding beta-subunit of rat p21-ras farnesyltransferase, the counterpart of yeast dpr1/ran1		
	JOURNAL MEDLINE	Cell 66, 327-334 (1991)		
	FEATURES	91309145		
	source	Location/Qualifiers		
	CDS	1..2464 /organism="Rattus norvegicus" /strain="Sprague-Dawley" /db_xref="taxon:10116" /tissue-type="brain" 60..1373 /codon_start=1 /product="farnesyl-protein transferase beta-subunit" /protein_id="AAA1176.1" /db_xref="GI:204186" /translation="MASSSSFTYYCPSPSSVFWSEPLYSLRPEHARELRLODVSERYVT SIEPAKVEEKIQEVSSYKYENHLVPRIVLQREKHFLRKRLROITDAYECIDRSALNAP LCWYLHSLELDDEPIQIVATDVCOPLFCOSPDGGCGPGGYPHILAPYAAYNA PDIETEEYAVYNIREKLLOYLSLKOPDGSLIMVGEDVDVRSVCAASVALNIIT CDLFEETAEWIAIRCONMEGGIGXPCGHADHGTYFFCGAALVIILAKRESLSMLKSLQW VTSOMRPBGCFGRCKNLVDGCTSFWMAGLLPLHLRALHAGGPDAUSMSHWFHQA LQEELIMCCQCPAGGLDDPKSRDFHTVCYCISGLSIQHFGSGAMLDHVDMGVPE VLPOTHEPVYNGPRKVQIATTHFLQKKVPPGEPECEDAVTSDPATD"		
	BASE COUNT	556 a 705 c 630 g 573 t		
	ORIGIN			
	Query Match	15.2% Score 206.6; DB 10; Length 2464;		
	Best Local Similarity	56.7%; Pred. No. 1.le-43;		
	Matches 402; Conservative	0; Mismatches 304; Indels 3; Gaps 1;		
	QY	172	AMGCAGAGCTGTGCGCGATGACATGCGATGCTGAGCCCTGGGCTGAGGCATATG	231
	Db	267	AGGCTCGTTCTTGCAAGAGGAGACGACTTCCATTATCTGAAAAAGAGGCTTCGACAACTG	326
	QY	232	GGACCAGCCCTTTCATGTTCTAGATGCCAATCCGCTTGCTATGCTAGTGATGTTGAT	291
	Db	327	ACAGATGCCCTATGATGTCTGATGATCCAGCGCCCCCTGCTGCTACTGATCTCGCAC	386
	QY	292	CCACTTGGTTCCTGATGAAGCACTTGATGATCTTTGAGATGATATCATAGACTTC	351

QY	352	TTACCTGCATGCAAGATTAAGATAGTGTGATATATGTGGACCTGGACATGTGCTCTAC	411
Db	387	AGCTTGGAGCTCCTCGAGGAACCCATCCCCCAAAATAGTGGCTACAGATGTGTCACTTC	446
QY	447	TTGGAGCTGTGTCAAGTCCAGACCGTGGCTTTGGAGGGGGCCCTGGTCAATCCACAC	506
QY	412	CTAGCTAGACATTAATGCTGTAAATACACTTGTGACAAATAGGAGCGAAAGACATTG	471
Db	507	CTCGCTCCAGCATGACAGTGTCTCAACGGCGATATGCATCATATTGGACAGGAGAACCTAC	566
QY	472	TCATCATCATATAGGGGACACCTGTACAAATTTTATGCTGCAGATGAAGAATGTACAGT	531
Db	567	AACGTCAATTAAACAGAGAAAGCTCCCTCAGTACCTTGTACTCCCTAAACCAACCGATGGC	626
QY	532	GCTTTACAGAAATGCATGATGTGGCCAAATGTAGTCCGTCTCTTCCCTACACCGCATTTACG	591
Db	627	TCTTTTTCATGACAGCTGTGGAGGAGAGGTGATGTAAAGAGTGGCTACTGTCTCGCTCA	686
QY	532	GTTGCCACGCTTGTGAAATATCTTGTATTTTAAACTGCGCAAAAGGTGTAGCGACTACATA	651
Db	687	GTAGCTCTCTCACCACACATCATCTACTCCTGACCTCTTGGAAAGGCACTGTGAATGATTA	746
QY	652	GCAACATGTCAAACTTATGAAGGTGTATGTGGGGAGCCCTTATGCTGAACACATGAT	711
Db	747	GCAAGGTCCCAACTGGGAAGGCGGCATTTGGCGGGGTGCCAGAGATGMAAGCCACGGT	806
QY	712	GGGTATACATTCCTGTGATTTGGCTCTTTGATCTGCTTAATGAGGACAGAAAGTTGAC	771
Db	807	GGCTACACCTTCTGTGGCTGTGGCTGCGCTGGATCTCTCAAGAAAGAAAGCTTCTTTGAAC	866
QY	772	TTGGCTACTTTGATTTGGCTGGCTGGCTTTTGTCTCA--AGAGTGGAAATGGCGATTTTCA	828
Db	867	CTGAAGACCTTGCTACAAATGGGTGAACAGCCGGCAGATGCGGTTGCAAGAGAGATTTTCA	926
QY	829	GGAGCAACATTAATAATGTTGATGTTGCTACTCTCTTTGGCAGGAG	877
Db	927	GGCGCTGCACAAAGCTGTGTGAGCGGCTGCTACTCTCTGTGCGCAGCGAG	975
RESULT 10			
LOCUS	ARI02375	1413 bp	DNA
DEFINITION	Sequence 8 from patent US 6083917.		linear
ACCESSION	ARI02375		PAT 14-FEB-2001
VERSION	ARI02375.1	GI:12813173	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1413)		
AUTHORS	Brown,M.S., Goldstein,J.L., Reis,Y. and Masters,J.		
TITLE	Methods and compositions for the identification, characterization		
JOURNAL	and inhibition of farnesyltransferase		
FEATURES	Patent: US 6083917-A 8 04-JUL-2000;		
source	Location/Qualifiers		
	1..1413		
BASE COUNT	324 a 395 c 380 g 314 t		
ORIGIN			
Query Match	15.0%; Score 203.6; DB 6; Length 1413;		
Best Local Similarity	56.5%; Pred. No. 5.9e-43;		
Matches 399; Conservative 0; Mismatches 304; Indels 3; Gaps 1;			
QY	172	ATGCTAGAGCTGTGGCGGTGATCAGCATATCGAGTATCTGACGCGCTGGCGCTGAGCATATG	231
Db	265	AGGCTCGTTTGGCAGAGGGAGACCACTTCATATCTGAAAAGAGGCGCTTCGACACATG	324
QY	232	GGACAGACCTTTTCATGCTCTAGATGCCAAATGGCCCTTGGCTATGCTAGCGTGTTCAT	291
Db	335	ACAGATGCCATATGATGTCTGTGATGCCAGCGCCCATGAGGCTCTGCTTATTTGATCTTGCAC	384
QY	292	CCACTGTCTTGTGATGAAGCACTTGAATGATCTTTGAAATGATATCATAGACTTC	351

Db 385 AGCTTGAGACGTGCTAGATGGAACCATCCCAATAGTGGCTACAGATGCTGTCAGTTTC 444  
QY 352 TTAGCTGATGATGAGATGAAGATGATGATAGTGGTGGACCTGACAGTTGCCCTCAC 411  
Db 445 TTGGAGCTGTGTGACAGCCCAAGAGTGGCTTTGGAGAGAGACCCGCTCAGTATCCAC 504  
QY 412 CTAGCTACGACTTATGCTGTGTAATATACCTGTGCAATPAGGAGCGAAGAGCATTTG 471  
Db 505 CTTCACACCCACATATGACAGCAATGATGATGATGATGATGATGATGATGATGATGAT 564  
QY 472 TCATCATCATATGAGGCAACCTGATACATTTATGCTGCAAGATGAAAGATGATCAGT 531  
Db 565 GACATCATTTAAG 624  
QY 532 GCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
Db 625 TCCTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684  
QY 592 GTTGCAGCCTTGTGATATTTCTGATTTTAACTGGCAAAAGGTGAGCGACTACATA 651  
Db 685 GTAGCCTGCTGACCAACATCATCATCTCCAGACCTTTTGAAGGCACTGCTGAATGATA 744  
QY 652 GCAAGATGTCAAACTTATGAAGGTGATGATGATGATGATGATGATGATGATGATGAT 711  
Db 745 GCAAGGTGTGAG 804  
QY 712 GGGTATACATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771  
Db 805 GGGTATACCTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 864  
QY 772 TTGCTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
Db 865 TTGAAGAGCTTATATCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 924  
QY 829 GGAAGCACTAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 874  
Db 925 GGGCGCTGCAACAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 970

RESULT 11  
LOCUS AR048524 1314 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 9 from patent US 5821118.  
ACCESSION AR048524  
VERSION AR048524.1 GI:5970867  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1314)  
AUTHORS Omer,C.A., Diehl,R.E., Gibbs,J.B. and Kohl,N.E.  
TITLE Genes for the subunits of human farnesyl-protein transferase  
JOURNAL Patent: US 5821118-A 9 13-OCT-1998;  
FEATURES  
source 1..1314  
BASE COUNT 300 a 361 c 361 g 292 t  
ORIGIN

Query Match 14.9%; Score 202; DB 6; Length 1314;  
Best Local Similarity 56.4%; Pred. No. 1.6e-42;  
Matches 398; Conservative 0; Mismatches 305; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGCTGATCAGCATATGATGATGATGATGATGATGATGATGATGAT 231  
Db 208 AGGCTTGTGTTGAG 267  
QY 232 GGACCAACCTTTATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 291  
Db 268 ACAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 327  
QY 292 CCACTTCTTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 351

Db 328 AGCTTGAGACGTGCTAGATGGAACCATCCCAATAGTGGCTACAGATGCTGTCAGTTTC 387  
QY 352 TTAGCTGATGATGAGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 411  
Db 388 CTGAGCTGTGTGACAGCCCAAGAGTGGCTTTGGAGAGAGACCCGCTCAGTATCCAC 447  
QY 412 CTAGCTACGACTTATGCTGTGTAATATACCTGTGCAATPAGGAGCGAAGAGCATTTG 471  
Db 448 CTTCACACCCACATATGACAGCAATGATGATGATGATGATGATGATGATGATGATGAT 507  
QY 472 TCATCATCATATGAGGCAACCTGATACATTTATGCTGCAAGATGAAAGATGATCAGT 531  
Db 508 GACATCATTTAAG 567  
QY 532 GCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
Db 568 TCCTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627  
QY 592 GTTGCAGCCTTGTGATATTTCTGATTTTAACTGGCAAAAGGTGAGCGACTACATA 651  
Db 628 GTAGCCTGCTGACCAACATCATCATCTCCAGACCTTTTGAAGGCACTGCTGAATGATA 687  
QY 652 GCAAGATGTCAAACTTATGAAGGTGATGATGATGATGATGATGATGATGATGATGAT 711  
Db 688 GCAAGGTGTGAG 747  
QY 712 GGGTATACATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771  
Db 748 GGGTATACCTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807  
QY 772 TTGCTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
Db 808 TTGAAGAGCTTATATCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 867  
QY 829 GGAAGCACTAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 874  
Db 868 GGGCGCTGCAACAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 913

RESULT 12  
LOCUS HUMPTB 1582 bp mRNA linear PRI 12-JUN-1993  
DEFINITION Human farnesyl-protein transferase beta-subunit mRNA, complete cds.  
ACCESSION L00635  
VERSION L00635.1 GI:292032  
KEYWORDS farnesyl-protein transferase; farnesyl-protein transferase beta-subunit.  
SOURCE Homo sapiens placenta cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1582)  
AUTHORS Omer,C.A.  
TITLE Characterization of recombinant human farnesyl-protein transferase: cloning, expression, farnesyl diphosphate binding and functional biochemistry with yeast prenyl-protein transferases  
JOURNAL Biochemistry (1993) in press  
FEATURES  
source 1..1582  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/lssue="type="placenta"  
20..1333  
/codon\_start=1  
/product="farnesyl-protein transferase beta-subunit"  
/protein\_id="AA35854.1"  
/translation="MSPSSFTYTPSPSSPVNSEPLYSLRPEHARELDDSVETVT  
SIOARVEKIDQEVSSYKFNHLYPRVLVLRKHNFYLRGLDLDAECIDASRPW  
LCWILHSLELDLDEPIQJIVATVCOFLQSCSPREGFGSGPOYHIALPYAAVAL  
CIIGTEADVIDINREKLQYISLRQDSFLMHVGEVDVRSAYCAASVASITNIT  
PDLFEETAEIRACQWMBEGISGVPEMEAHGCTTFCGLAALVILKRESLNLSLQW



QY	412	CTGACGTAGACCTTTGCGTGTGTAATACACTTGTGCAATATAGGAGCGAAAGACATTG	471
Db	463	CTTGACACCCACATATGACGACAGCTCAATGCTATTGTGCATTCATTGGCACCAGAGAGCCATAT	522
QY	472	TCATCATCAATATAGGCGCAACCTGTACAAATTTTATGCTGCAGATGAAGAATGTATCAGGT	531
Db	523	GACATCATTTAACAGAGAAACACTTCCTTCAGTATTTGTACTCCCTGAAACCAACTGTACGCC	582
QY	532	GCTTTGACAAGATGCATGATGGTGGCGCAAAATGTATGTCCTGCTTCCCTACACCGCTATATCG	591
Db	583	TTCCTTTCTCATGACATGTGCGAGGTAGGTGATGTGAAGACGCACTTACTGTGCTGCCCTCC	642
QY	592	GTTGCGACACTTGTGTAATATTCCTGATTTTAACTGCGCAAAAGGTGTAGGCGACTACATCA	651
Db	643	GTAGCGCTGCGTACACCAATCATCTACCTCCAGACCTCTTTGAGGGGCACTGTGAATGATGA	702
QY	652	GCAAGATGTCAAACTTATGAAAGGTGTATTGTCTGGGGAGCCTTATGTGTAAGCACATGCT	711
Db	703	GCAAGGTGTCAAGAACTGGGAAAGGTGGCAATTTGGCGGGGTACCAAGGAGATGAAAGCCCATG	762
QY	712	GGGTGTACATTCCTGTGGAATGGCTGCTTTGATTCCTGCTTAATGAGCGAGAGAAAGTTGAC	771
Db	763	GGGCTTACCTTTCTGTGGGCTTGCCCGCCGCTGGTAATCCTCCMAAGAGGAACCTTCCCTTGAC	822
QY	772	TTGCGCTACTTGTGATGGCTGGGTGGCTTTTGTCTCA--AGGAGTGGAAATGCCGATTTTCAA	828
Db	823	TTTGAAGACCTTATTTCAATATGGGTGGTGCACAGCGCGAGATGCATTTTGAAGAGGATTTTCAG	882
QY	829	GGAGCAACTAATTAATTTGGTTGATGGTTGAGTCACTCCTTTGGCCAG	874
Db	883	GGCCGCTGCAACCAAGCTGGTGGATGGCTGCTACTCCTTCTGGCAGG	928

RESULT	14
LOCUS	AR077273
DEFINITION	AR077273 1248 bp DNA linear PAT 31-AUG-2000
ACCESSION	Sequence 8 from patent US 5962243.
VERSION	AR077273
KEYWORDS	AR077273.1 GI:10004019
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1248)
TITLE	Brown,M.S., Goldstein,J.L. and James,G.L.
JOURNAL	Methods for the identification of farnesyltransferase inhibitors
FEATURES	Patent: US 5962243-A 8 05-OCT-1999;
source	location/Qualifiers 1..1248 /organism="unknown"
BASE COUNT	286 a 285 t
ORIGIN	339 c 338 g

Query Match	14.7%;	Score 200.4;	DB 6;	Length 1248;
Best Local Similarity	-56.2%;	Pred. No. 4.1e-42;		
Matches 397;	Conservative 0;	Mismatches 306;	Indels 3;	Gaps 1;

[illegible]

Oy 412 CTGATGACGACATATGCGCTGTAAATACACTGTGACAATAGGGAGCAAAAGACATTG 471  
 Db 298 CTTGCAACCACATATGCAAGCACTCAATGATTTGTCTATCATATGGCAACCGAGAGGCCATT 357  
 Oy 472 TCTCATCATCAATAGGGGCAACCTGTACAAATTTTATGCTGCAGATGAAGAATGTATACGT 531  
 Db 358 GACATCATTAACAGAGAGAGAGCTTCTCAGTATTGTACTCCCTGAAACACCTGACGGC 417  
 Oy 532 GCTTCACAGATGCAATGATGATGTGGCAAAATTGATGTCCGTGCTTCTACACCGCTATATCG 591  
 Db 418 TCCCTTCATGACATGCTGGAGGTGAGGTGAGTGTGAAAGAGCGCATCTGTGCCCTCC 477  
 Oy 592 GTTGGCAGCCCTGTGAATATTCTGTATTTTAACTGCGCAAAAGTGTAGCGACTATACATA 651  
 Db 478 GTAGCGCTGGCTGACCAACATCATCACTCCAGACCTCTTTGAGGGCAACGTGTAAATGATTA 537  
 Oy 652 GCACAGTGTCAAACTTATGAGAGGTGGTATGTCTGGGAGACCTTATGCTGAGACACATGCT 711  
 Db 538 GCACAGTGTCAAACTGAGAGGTGGTATGTCTGGGAGACCTTATGCTGAGAGACACATGCT 597  
 Oy 712 GGGTATACATTTGTGAGATTTGCTCTTGTGATCTGCTTAAATGAGAGCAAGAAACTTGAC 771  
 Db 598 GGCTATTACCTTCTGTGGCCCTGGCCGGCGCTGTGTAATCTCTCAAGAGGGAACGTTCCCTTGAAC 657  
 Oy 772 TTGCTTACTTTGATTTGGCTGGGTGGCTTTTCGTCA --AGGAGTGGAAATGCGGATTTTCAA 828  
 Db 658 TTGAGAGAGCTTTTCAAAATGAGGTGACAAAGCCGGCAGATGCTATTGTAAGAGAGATTTTCAG 717  
 Oy 828 GGACGACATCAATAATTTGGTGTGATGGTGTCTCTCTTTGGCAGG 874  
 Db 718 GGCCCGCTGCACAACTGGTGGATGGCTGTCTTACTCTTCTGTGGCAGG 763

RESULT	15				
LOCUS	112222	1248 bp	DNA	linear	PAT 26-JUL-1995
DEFINITION	Sequence 8 from patent US 5420245.				
ACCESSION	112222				
VERSION	112222.1	GI:909720			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1248)				
AUTHORS	Brown,M.S., Goldstein,J.L. and Reiss,Y.				
TITLE	Tetrapeptide-based inhibitors of farnesyl transferase				
JOURNAL	Patent: US 5420245-A 8 30-MAY-1995;				
FEATURES	Location/Qualifiers				
SOURCE	1..1248				
	/organism="unknown"				
BASE COUNT	286 a 339 c 338 g 285 t				
ORIGIN					

Query Match	14.78;	Score 200.4;	DB 6;	Length 1248;
Best Local Similarity	56.28;	Pred. No. 4.1e-42;		
Matches 397;	Conservative 0;	Mismatches 306;	Indels 3;	Gaps 1;

QY	172	ATCTAGAGCTGTGGCCGTGATCACATATCGATATGTGACCGCTGGGCTGAGGCATATG	2311
Db	58	AGGCTGTGTTTTGCAGAGGAGGAGAACACTCTCCATTATGTGAAGAGGCTTCGACAACTG	117
QY	232	GGACCAAGCCTTTCATGTTCTCTGATGAGCCCATGCGCCCTTGCGCTACTGATGATGTCAT	2911
Db	118	ACAGATGCCCTTAGTGTCTGGATGTCGAGCGCCCATGAGCTCTGCTATTGGAATCTCGAC	177
QY	292	CCACTTGGCTTTCGTGATGAAGCACTTGATGATGATCTTGAGAAATCATAGACTTC	3511
Db	178	AGCTTGAAGACTGTAGATGATGAAACCATCCCCACATAGTGGCTACAGATGTTGTCTGAGTTC	237
QY	352	TTAGCTGCATGTCAGAGATAAAGATGGTGTGATATAGTGTGGACTGCAACGTTGCTCAC	4111
Db	238	CTGGAGCTGTGTTCAGAGCCCGAAGAGGTGGCTTTGGAGAGAGACCCGCTGAGTATTCACAC	297





DR WPI: 2000-256964/22.  
 DR P-PSDB; AAY70502.  
 XX  
 PT New isolated polynucleotide encoding farnesyltransferase polypeptide is  
 PT useful for producing transgenic plants with an altered level of  
 PT farnesyltransferase -  
 PS  
 XX Claim 3: Page 38-39; 51pp; English.  
 XX  
 CC The present sequence is a cDNA encoding farnesyltransferase beta subunit  
 CC from clone p0127.cdnb.1br isolated from corn nucellus tissue  
 CC cDNA library. The present sequence is used in the construction  
 CC of a chimeric gene to produce transgenic plants with altered level  
 CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase  
 CC activity may have enhanced tolerance to drought stress. Nucleic acids  
 CC encoding all or a part of farnesyltransferase proteins can be used in  
 CC studies to understand cell growth in plants and provide genetic tools to  
 CC control cell growth and improve tolerance to drought in mature plants.  
 XX  
 SQ Sequence 1359 BP: 340 A; 308 C; 351 G; 360 T; 0 other;

Query Match 100.0%; Score 1359; DB 21; Length 1359;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACCCCTCCCGCAGTCGACCGCCGCCAGAGAGACCCGCGCGCGGAT 60  
 DB 1 ATGAGACCCCTCCCGCAGTCGACCGCCGCCAGAGAGACCCGCGCGCGGAT 60  
 QY 61 CCCGACCTACGAGGCTGACGAGTACGAGTACGAGTACGAGTACGAGTACGAGT 120  
 DB 61 CCCGACCTACGAGGCTGACGAGTACGAGTACGAGTACGAGTACGAGTACGAGT 120  
 QY 121 GCGCAGATCTACCGCTCTTTCGCGCGCGCGCCCAAGCAAGAAATCATGCTAGAG 180  
 DB 121 GCGCAGATCTACCGCTCTTTCGCGCGCGCGCCCAAGCAAGAAATCATGCTAGAG 180  
 QY 181 CTGCGGCTGATCAGATATCGAATATCTGACGCTGGCTGAGGCAATGGACCGCC 240  
 DB 181 CTGCGGCTGATCAGATATCGAATATCTGACGCTGGCTGAGGCAATGGACCGCC 240  
 QY 241 TTTGATGTTGATGCAATCGCCCTTGGCTATGCTACTGATGATGCTACTGCT 300  
 DB 241 TTTGATGTTGATGCAATCGCCCTTGGCTATGCTACTGATGATGCTACTGCT 300  
 QY 301 TTTGATGTTGATGCAATCGCCCTTGGCTATGCTACTGATGATGCTACTGCT 360  
 DB 301 TTTGATGTTGATGCAATCGCCCTTGGCTATGCTACTGATGATGCTACTGCT 360  
 QY 361 TGTAGAGATAAAGATGATATAGTGTGAGACCTGGACAGTTGCTCAGCTAGC 420  
 DB 361 TGTAGAGATAAAGATGATATAGTGTGAGACCTGGACAGTTGCTCAGCTAGC 420  
 QY 421 ACTATGCTGCTGTAATACACTTGTGACAATAGGAGGCAAGAGATGCTCATC 480  
 DB 421 ACTATGCTGCTGTAATACACTTGTGACAATAGGAGGCAAGAGATGCTCATC 480  
 QY 481 AATAGGCGCAACCTGTACAAATTTTATCTCAGATGAAGAATGATAGGTGCTT 540  
 DB 481 AATAGGCGCAACCTGTACAAATTTTATCTCAGATGAAGAATGATAGGTGCTT 540  
 QY 541 ATGATGATGATGCGCAAAATTTGATGCTCGTCTTCTACACCGCTATATCG 600  
 DB 541 ATGATGATGATGCGCAAAATTTGATGCTCGTCTTCTACACCGCTATATCG 600  
 QY 601 CTCTGATATATCTTGAATTTTAACTGGCAAAAGGTGAGGCACTACATAGCA 660  
 DB 601 CTCTGATATATCTTGAATTTTAACTGGCAAAAGGTGAGGCACTACATAGCA 660  
 QY 661 CAACCTATAGAGGTGATTTGCTGGGAGCCTTATGCTGAGACATATGGTGGT 720  
 DB 661 CAACCTATAGAGGTGATTTGCTGGGAGCCTTATGCTGAGACATATGGTGGT 720

QY 721 TTCTGATGATGCTGCTTGTGATCTGCTTATATAGGACAGAGAAAGTACCTGCTAGT 780  
 DB 721 TTCTGATGATGCTGCTTGTGATCTGCTTATATAGGACAGAGAAAGTACCTGCTAGT 780  
 QY 781 TTGATGCTGCTGCTGCTTGTGCTCAAGAGAGTGAATGCGGATTTAGAGCACTAAT 840  
 DB 781 TTGATGCTGCTGCTGCTTGTGCTCAAGAGAGTGAATGCGGATTTAGAGCACTAAT 840  
 QY 841 AAATGCTGATGCTGCTGCTGCTTGTGCTCAAGAGAGTGAATGCGGATTTAGAGCACTAAT 900  
 DB 841 AAATGCTGATGCTGCTGCTGCTTGTGCTCAAGAGAGTGAATGCGGATTTAGAGCACTAAT 900  
 QY 901 TTAATTAAGATTTGTAAGAATTAAGAACTGCTGATTTCTGCAAAAGCCATCAGCA 960  
 DB 901 TTAATTAAGATTTGTAAGAATTAAGAACTGCTGATTTCTGCAAAAGCCATCAGCA 960  
 QY 961 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB 961 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1021 GACTATGCGAAGTTGATTTGATTTATACACAGAGCAACCAATGCGCCACTCTTC 1080  
 DB 1021 GACTATGCGAAGTTGATTTGATTTATACACAGAGCAACCAATGCGCCACTCTTC 1080  
 QY 1081 CATTAACATTTGCTGCAACAAATACATCTACTTGTCTCAGTACTAGAGGAGCTTG 1140  
 DB 1081 CATTAACATTTGCTGCAACAAATACATCTACTTGTCTCAGTACTAGAGGAGCTTG 1140  
 QY 1141 AGGATTAAGCTGTAAGAAAGACAGATCACTATCAATTCATGCTAGTGCCTGCTGCT 1200  
 DB 1141 AGGATTAAGCTGTAAGAAAGACAGATCACTATCAATTCATGCTAGTGCCTGCTGCT 1200  
 QY 1201 GCAGTTAGCCAGTACAGTGCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 DB 1201 GCAGTTAGCCAGTACAGTGCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 QY 1261 CTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 DB 1261 CTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 QY 1321 AAGTACCATACAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 DB 1321 AAGTACCATACAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

RESULT 2  
 ID AA51792 standard; cDNA: 1031 BP.  
 XX AA51792:  
 AC 04-JUL-2000 (first entry)  
 DT  
 XX  
 DE Rice farnesyltransferase beta subunit cDNA.  
 XX  
 KW Rice; farnesyltransferase beta subunit; transgenic plant;  
 XX drought tolerance; cell growth; ss.  
 OS  
 XX Oryza sativa.  
 XX  
 FH Key Location/Qualifiers  
 FT 91..1029  
 FT /tag- a  
 FT /product- "Farnesyltransferase beta subunit"  
 FT /note- "does not include stop codon"  
 FT /partial  
 XX  
 PD WO200014207-A2.  
 XX 16-MAR-2000.  
 XX  
 PF 07-SEP-1999; 99WO-US20419.  
 XX



PR 08-SEP-1998: 98US-0099521.  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
PA Cahoon RE, Miao G, Powell W;  
XX MPI: 2000-256964/22.  
XX P-PSDB; AA170503.  
XX New isolated polynucleotide encoding farnesyltransferase polypeptide is  
PT useful for producing transgenic plants with an altered level of  
PT farnesyltransferase -  
XX  
XX Claim 3: Page 40-41; 51pp: English.  
XX  
XX The present sequence is a cDNA encoding farnesyltransferase beta subunit  
CC from clone rlr24.pk0007.d6 isolated from rice infected leaf  
CC CDNA library rlr24. The present sequence is used in the construction  
CC of a chimeric gene to produce transgenic plants with altered level  
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase  
CC activity may have enhanced tolerance to drought stress. Nucleic acids  
CC encoding all or a part of farnesyltransferase proteins can be used in  
CC studies to understand cell growth in plants and provide genetic tools to  
CC control cell growth and improve tolerance to drought in mature plants.  
XX  
XX Sequence 1031 BP; 228 A; 249 C; 302 G; 252 T; 0 other:  
SQ  
Query Match 45.1%; Score 613; DB 21; Length 1031;  
Best Local Similarity 84.1%; Pred. No. 9,7e-180;  
Matches 704; Conservative 0; Mismatches 130; Indels 3; Gaps 1;  
OY 57 GGATCCCGACCTACCGAGCTGACGAGTGAGCGAGTGAGCAGATGAGGAGGCCAG 116  
DB 168 GCGCGGTGAGCTGCGCCGCTGACTGTGACGAGTGAGCAGATGAGGAGGCCAG 227  
OY 117 GGTGGGAGATACCGCTCCCTCTGCGGGGCGCGCCCAACAGCAATTCATGATGCT 176  
DB 228 GGTGGGAGATACCGCTCCCTCTGCGGGGCGCGCCCAACAGCAATTCATGATGCT 287  
OY 177 AGAGCTGTGCGTGAGCAGATATGAGATCTGACGCGCTGCGCTGAGCAGCATATGAGC 236  
DB 288 AGAGCTGTGCGTGAGCAGATATGAGATCTGACGAGGCGCTGAGCAGCATATGAGC 347  
OY 237 AGCCTTCATGTTCTAGATGCGCAATGCGCCTTGCTATGCTACTGATGCTTCATGCT 296  
DB 348 AACCTTCATGTTCTAGATGCGCAATGCGCCTTGCTATGCTACTGATGCTTCATGCT 407  
OY 297 TGGCTTGGAGATGAGCAGCTGATGATGATCTTGAGCAATGATATCATGCTTATG 356  
DB 408 TGGCTTGGAGATGAGCAGCTGATGATGATCTTGAGCAATGATATCATGCTTATG 464  
OY 357 TCGATGTCAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 416  
DB 465 TCGATGTCAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 524  
OY 417 TACGACTTATGCTGCTGTAATACACTTGTGACATAGGAGCGAAGACCATTTGATC 476  
DB 525 TACGACTTATGCTGCTGTAATACACTTGTGACATAGGAGCGAAGACCATTTGATC 584  
OY 477 AACCAATAGGAGGACCTGTACAAATTTATGTCGATGATGATGATGATGATGATG 536  
DB 585 GGTAAACAGGAGCAACCTGTACAAATTTATGTCGATGATGATGATGATGATGATG 644  
OY 537 CAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 596  
DB 645 CAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 704  
OY 597 CAGCTTGTAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 656  
DB 705 CAGCTTGTAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 764  
OY 657 ATGCAACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 716

DB 765 GTGTCAAACTATGAGAGTGATGCTGCGGGAACCTATGCTGAACTATGCTGCTA 824  
OY 717 TACATTCGTGATATGAGCTGCTGCTGATCTGCTTAAATGAGCAGAGAACTGATGCC 776  
DB 825 CACTTTTGTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 884  
OY 777 TACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836  
DB 885 TACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944  
OY 837 TAAATTAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 993  
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RESULT 3  
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ID AA251793 standard; cDNA; 1504 BP.  
XX  
XX AA251793;  
XX  
XX 04-JUL-2000 (first entry)  
XX  
XX Soybean farnesyltransferase beta subunit cDNA clone sfl1.pk0086.h10.  
XX  
XX Soybean; farnesyltransferase beta subunit; transgenic plant;  
KM drought tolerance; cell growth; clone sfl1.pk0086.h10; ss.  
XX  
XX Glycine max.  
XX  
XX Key Location/Qualifiers  
FH CDS 63..1352  
FT /\*tag- a  
FT /product- "Farnesyltransferase beta subunit"  
XX  
XX W0200014207-A2.  
XX  
XX 16-MAR-2000.  
XX  
XX 07-SEP-1999; 99MO-US20419.  
XX  
XX 08-SEP-1998; 98US-0099521.  
XX  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
XX Cahoon RE, Miao G, Powell W;  
XX MPI: 2000-256964/22.  
XX P-PSDB; AA170504.  
XX  
XX New isolated polynucleotide encoding farnesyltransferase polypeptide is  
PT useful for producing transgenic plants with an altered level of  
PT farnesyltransferase -  
XX  
XX Claim 3: Page 42; 51pp: English.  
XX  
XX The present sequence is a cDNA encoding farnesyltransferase beta subunit  
CC from soybean clone sfl1.pk0086.h10.  
CC The present sequence is used in the construction  
CC of a chimeric gene to produce transgenic plants with altered level  
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase  
CC activity may have enhanced tolerance to drought stress. Nucleic acids  
CC encoding all or a part of farnesyltransferase proteins can be used in  
CC studies to understand cell growth in plants and provide genetic tools to  
CC control cell growth and improve tolerance to drought in mature plants.  
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Query Match 36.1%; Score 491.2; DB 21; Length 1504;  
Best Local Similarity 61.8%; Pred. No. 8.8e-142;  
Matches 815; Conservative 0; Mismatches 473; Indels 30; Gaps 1;  
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Oy 130 TACGGCTCCCTTCGCGGGGCGCCGCAACAGAAATCCATCATGCTGACCTGGGGT 189
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Oy 190 GATCAGCATATGAGATCTGAGCCCTGGGCTGAGGCAATATGGAGCAGCCCTTCATGTT 249
Db 150 GATATATCATGATGATATGCTCCAAAGGCTTCGCCATCTCAGTCCGAGCTTTCCGCTT 209
Oy 250 CTACATGCCATCGCCCTTGGCTATGCTACTGATGGTTCATCCACTTGCCTTCTGGAT 309
Db 210 TTGAGAGCTAATCGACCCCTGGCTGCTACTGATCTTCCACTCCATTCCTTTTCCGGA 269
Oy 310 GAACGACTTGTAGATCTTGAGAAATGATATCATAGACTCTTAAGCTGATGTAGAT 369
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Oy 370 AAAGATGGTGAATATAGTGTGAGCTGGAGAGTTGCCCTCAGCTAGCAGCTTATGCT 429
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Oy 610 ATTCTTATTTTAACTGCGCAAAAGCTGTAGCCACTATAGCAAGATGTCAACTTAT 669
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Db 630 GAGGTGGCATTTGCTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
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Oy 850 GATGTTGCTACTGCTTTGCGAGGAGCTGCTGCTTTCAGACAAATTAATTAATG 909
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Db 870 ATTATCAACAAGAGATGAGAGACATCAAGATTTTGGGATGATCTTATGATCTGAA 929
Oy 970 TGCAGCAGCAGTTCATATGGGTGACCGCGAAGAAAGCTTCCCTGCTGCTGCTGCTGCTGCT 1020
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Oy 1021 -----GACTATGCAAGTTGGATTTGATTTTATCAACAGAGC 1059
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Oy 1060 AACCAAAATGGCCAGCTTTCATTAACATTAACATTAACATTAACATTAACATTAACATTAACAT 1119
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Db 1110 CAGGAGCAAGAGGGTGACTGAGAGACAAACCGGTAACGTATAGATCATTTATCACACA 1169
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Oy 1240 TGCCCATACCTCAGCATGCTGCTTGGACCGTACTCTAATTTGCTGAGCCCAATCCATCA 1299
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Db 1290 CTCCTTAATGTTGCTTGGAGCATATTCGTAACCTCATGAAATTCCTTACTGAGT 1347

RESULT 4
AAC35019
ID AAC35019 standard; DNA; 1525 bp.
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AC AAC35019;
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DT 17-Oct-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 8713.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
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QY 601 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
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DB 1424 G 1424

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XX  
DT 18-OCT-2000 (first entry)  
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW Protein Identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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XX  
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QY	124	GACATCTAACCGCTCCCTCTTCGGGGCCGCCCCCAACAAGAAATTCATCTCTAGAGCTC	183
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QY	244	CATGTTCTAGATGCCAATCGCCCTTGGCTATGCTACTGAGATGGTATCTCCACACTTGGTTTG	303
Db	187	TCTTCCTTAGATGCTAATCGACCTTGGCTTGTACTGAGATCTTCAATTCATATAGCTTTG	248
QY	304	CTGAGTAAAGCACTTGATGATGATCTTGGAGATGATATCATATAGACTTCTTAACCTGATGT	363
Db	247	CTTGGGAGAGCTGGATGATGATTAATTAAGAAAGCAATCCCATGTGACTCTTGGACGCTGC	306
QY	364	CAGGATTAAGATGGTGGATATAGTGGAGGAGCTGGAGATGGCTCCACAGCTAGCACACT	423
Db	307	CAGGAGCTCTGAAGTGGATACGGTGGTGGCTGGCCCACTTCACACTCTTGGCAACTACT	366
QY	424	TATGCTGCTTAATTAATACACTTGTGACAAATAGGAGCGCAAGGACATTTGATCAATCAAT	483
Db	367	TATGCTGACAGTATGCACTGTACTTTAGAGGTGCAAAAGCCCTTCTTCAATTAAT	420
QY	484	AGGGGC-----AACCTGTACAATTTTATGCTGACAGATGAAA	519
Db	427	AGGGGTGATCTCTTTTTTCTTGTGAGAAAATATGCTTGTTTTAAACGCGATGAG	486
QY	520	GATATATCAGSTGCTTCAGAAATGCAATGATGGTGGCAATTTGATGCTCCCTGCTCTAC	579
Db	487	GATCAAGTGAAGTTCACAGATGCAATATGGAGAAATATGGATGCTCTGATGCTTAC	546
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Db	547	ACTGCATTTTCGGTTCGACAGATGCTTAATATTTATGATGATGATGACACACCCAGGCGTA	606
QY	640	GCGGACTACATACGACAGATGTCAAACCTATTAAGAGGTGCTATATGCTGGGAGCCTTATGCT	699
Db	607	GGAGATTACATCTTGACCTCCCAAACTTATGAAGGTGGCAATTGGAGGGAACCTGGCTCC	666
QY	700	GAGGACATGCTGGGCTATACATTCGTGGATATGGCTCCTTGTGATCCCTGCTTAATGAGCA	759
Db	667	GAACTCAGCGTGGATATACCTACTGCTGGTTGGCTGTACATTTTAAATCAATGAGGCTC	726
QY	760	GAGAAATGACTTGGCTTACTTGTGATTCGCTGGGTGGCTTTTGTCAAGGAGTGAATGC	819
Db	727	GAGCGTTGAATTTGATTTATTAATGAATATGGGCTGTACATGACACAGGAGTAGAANAAT	786
QY	820	GGAATTCAGGAGCAACTAATTAATGCTTGAATGCTTGAATGCTTCTTATCTTTGGCAGGAGCT	879
Db	787	GGATTTCAAGGTAGGAGCAAAATTTGGTGCATGTTGCTACACATTTTGGCAGGAGCC	846
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Db	847	CGTTGTGTTCTACTACAAAGATTATATCCAAACCATGATCATGAGTTCATGATCATCA	906
Oy	937	TATTCCTCGCAAAAGCCATCAGGAGGA-----TCCCTCC	972
Db	907	CATATATCAGAGGAGCAAAATGAAGAACATCATGCTCATGATGAAAGATGACCTTGAGAC	966
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Oy	1033	TTTGGATTGATTTTATACAAACAGAGCACCAATTGGCCCACTCTTCATATCAATTGCC	1092
Db	1037	ATTCATCATACATCCACCTCATTTAACAGGAGATGCCAACTGGTTTTCATAGCCTCGGC	1086
Oy	1093	CTCGAACAAATACATCCTACTTTGTCTCAGGTACTAGAGGAGGCTTGAGGATTAAGCT	1152
Db	1087	TTTGAGAGATATATGACTCTTGCTGCTCTAAGATCCCTGACAGGTGTGATTCCAGACAAAGCCG	1146
Oy	1153	GGAAAGAACAGAGATCACTATTCATTCATGCTACTGCTCAGTGGCCCTGCAAGTATGACCAG	1212
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Oy	1213	TACAGTGCATGACTGATCTACTGTTGGTGGCCCATTCACCTCAGACATGTGTTGGACCGTAC	1272
Db	1207	CACCGTTGGTTAAAGACGAGGACACTCCTCCTTTGACTCGGCAATTATGGGTGGCTAC	1266
Oy	1273	TCCTAATTGGTGGAGCCAAATCCATCCACTCTACAAATGTTGTCTAGATTAAGTACCATACA	1332
Db	1267	TGCAATCTCCCTTGAACTGTTCAAACTTTCACACACATGTGATGGATCAGTATTAATGAA	1326
Oy	1333	GCCTATGAGTTCTTCTCAGAG	1354
Db	1327	GCCTATGAGTTCTTCTTAAAG	1348

RESULT 7	
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ID	AAQ44398 standard; cDNA; 2464 BP.
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AC	AAQ44398;
XX	
DT	08-AUG-1994 (first entry)
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DE	Farnesyltransferase beta-subunit.
XX	
KM	Farnesyltransferase; FT; beta-subunit; p21ras; ras protein;
KW	cancer therapy; ss.
XX	
OS	Rattus sp.
XX	
PN	MO9404561-A.
XX	
PD	03-MAR-1994.
XX	
PF	24-AUG-1993; 93MO-U080062.
XX	
PR	24-AUG-1992; 92US-0935087.
XX	
PA	(GETH ) GENENTECH INC.
PA	(TEXA ) UNIV TEXAS SYSTEM.
XX	
PI	Brown MS, Goldstein JL, Masters JC, Reiss Y;
XX	
DR	WPI; 1994-083105/10.
XX	
DR	P-PSDB; AAR49740.
PT	New farnesyl-transferase inhibitors - used for inhibiting
XX	attachment of a farnesyl moiety to a p21ras protein in malignant
XX	cells
PS	Disclosure; page 123-25; 183pp; English.
CC	The cDNA (AAQ44398) and amino acid (AAR49740) sequences of rat





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Db 687 GTACCTCTCTCACCAACATCATCTACTCTGACCTCTTCGAAAGCAGCTGCTGAATGATA 746
Qy 652 GCAGATGTCAAACTTATGAGTGTATGCTGAGGAGCCTTATGCTGAAGCATATGT 711
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Db 747 GCAGGTGTCAGAACTGGAGAGGCGGATTTGGCGGATGCCAGGATGGAAGCCACAGGT 806
Qy 712 GGGTATACATTTCTGTGATGGCTGCTCTTTGCTTCTCTGCTTAATGAGCAGAAAGTTGAC 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 807 GGGTACACCTTCTGTGCTGGCTGGCTGCTGATCTCTCAAGAGAGAAAGCTTCTTCAAC 866
Qy 772 TTGCTAGTTTGGTGGCTGGCTTTTGTCTCA---AGAGTGAATGGCGATTTCA 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 867 CTGAAGAGCTTCTGACATGGGTACAAAGCCGAGATGCGGTTGCAAGAGAGATTTGAG 926
Qy 829 GGACGAACATAATAATGTTGATGTTGCTACTCTTTTGGCAGGAG 877
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 927 GGGCGTCTCAACAGCTGTGTGAGCGCTGCTACTCTTCTTGGCAGGAG 975

RESULT 9
AAT38709
ID AAT38709 standard; cDNA; 2464 BP.
XX
AC AAT38709;
XX
DT 30-JUL-1997 (first entry)
XX
DE Rat farnesyl transferase enzyme beta subunit cDNA.
XX
KM Farnesyl transferase; Inhibitor: cancer; tumour; neoplasia; prenyl;
KW ras protein; K-ras B; malignant; detection; identification; ss.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 59..1373
FT /tag= a
XX
PN WO9634113-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96MO-US05969.
XX
PR 27-APR-1995; 95US-0429964.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Brown MS, Goldstein JL, James GL;
XX
DR WPI, 1996-497642/49.
DR P-PSDB; AAM04428.
XX
PT Assay for farnesyl transferase activity - by determining ability to
PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
PT identifying inhibitors
XX
XX Example 3: Page 147-151; 257pp; English.
XX
XX AAT38709 encodes the beta subunit of a farnesyl transferase (FT) enzyme
XX derived from a rat brain cDNA library. The enzyme was used in a method
XX for identifying FT inhibitors. The method involved screening candidate
XX compounds for the ability to inhibit the transfer of a farnesyl moiety
XX to a K-ras B protein. FT inhibitors act by blocking the attachment of
XX prenyl groups to ras proteins in malignant cells of patients suffering
XX from cancer or precancerous states, and as such are used to treat such
XX conditions.
SQ Sequence 2464 BP; 556 A; 705 C; 630 G; 573 T; 0 other;

Query Match 15.2%: Score 206.6; DB 17; Length 2464;
Best Local Similarity 56.7%: Pred. No. 3.4e-53;
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;
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Qy 172 ATGCTAGAGCTGTGGCCGTGATCAGCATATGAGTATCTGACGCTGGGCTGAGCATATG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 AGCGTCGTTCTGCGAGAGGAGAAAGCACTTCATATCTGAAAGAGGCTTTCAGCAACTG 326
Qy 232 GGACCAACCTTTTCAATGTTCTAGATGCCATGCGCTTGGCTATGCTAGTGGATGTTGAT 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 ACAGATCCCTATGATGATGTGATGCCAGCGCCGCCCTGCTCTGCTGATCTGCTGAC 386
Qy 292 CCACTTCTTTTGTGATGAGGACCTGATGATGATGATGATGATGATGATGATGATGATG 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 387 AGCTTGAAGCTCTCTGCGAGAACCCATCCCCAAATATGCTGCTACATGTTGTCACTTC 446
Qy 352 TTAGCTGATGTCAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 447 TTGAGAGCTGTGACAGATCCAGACGAGTGGCTTTGAGAGGGGCGCTGCTAGTACCCAC 506
Qy 412 CTAGCTACGATTTATGCTGCTGTTAAATACACTTGTGACATAGGAGACGAAAGACTTG 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 507 CTGCTCCCAAGTATGAGCTGTCAACGCGCTATGCTATGCTATGCTACGAGGAGAGGCTTAC 566
Qy 472 TCATCAATCAATAGGGGCAACCTGTACAAATTTATGCTGCAAGATGAAAGATGATACAGT 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 567 AACGTCATTTAACAGAGAGAAAGCTCTTCAGTACTTCTACTCCCTTAAAGCAACCGGATGCC 626
Qy 532 GCTTTTCAGAAATGCATGATGATGCGGAAATGATGTCGCTCTTCTACACCGCTATATCG 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 627 TCTTTTCTCATGACGCTGCGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 686
Qy 592 GTTGGCCAGCCTTGTGATATTTCTGATTTTAACTGCGCAAAAGTGTAGCGCATACATA 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 687 GTAGCCTCTCTCACCAACATCATCTACTCTGACCTCTTCGAAAGCAGCTGCTGAATGATA 746
Qy 652 GCAGATGTCAAACTTATGAGTGTATGCTGAGGAGCCTTATGCTGAAGCATATGT 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 747 GCAGGTGTCAGAACTGGAGAGGCGGATTTGGCGGATGCCAGGATGGAAGCCACAGGT 806
Qy 712 GGGTATACATTTCTGTGATGGCTGCTCTTTGCTTCTCTGCTTAATGAGCAGAAAGTTGAC 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 807 GGGTACACCTTCTGTGCTGGCTGGCTGCTGATCTCTCAAGAGAGAAAGCTTCTTCAAC 866
Qy 772 TTGCTAGTTTGGTGGCTGGCTTTTGTCTCA---AGAGTGAATGGCGATTTCA 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 867 CTGAAGAGCTTCTGACATGGGTACAAAGCCGAGATGCGGTTGCAAGAGAGATTTGAG 926
Qy 829 GGACGAACATAATAATGTTGATGTTGCTACTCTTTTGGCAGGAG 877
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 927 GGGCGTCTCAACAGCTGTGTGAGCGCTGCTACTCTTCTTGGCAGGAG 975

RESULT 10
AA064888
ID AA064888 standard; cDNA; 1314 BP.
XX
AC AA064888;
XX
DT 07-NOV-1994 (first entry)
XX
DE cDNA encoding beta subunit of human FPTase.
XX
KM Farnesyl protein transferase; Inhibition: farnesylation; ss.
XX
OS Homo sapiens.
XX
PN WO9410184-A.
XX
PD 11-MAY-1994.
XX
PF 29-OCT-1993; 93MO-US10442.
XX
PR 30-OCT-1992; 92US-0968782.
XX
PA (MERI ) MERCK & CO INC.
```



QY 532 GCTTCGAATGCATGTCGCGCAAAATGATGTCCTGCTCTACACCGCTATATCG 591  
DB 418 TCCCTTCTCATGTCGAGGTGAGGTGATGTGAGAGCCGATCTGCTGCTCC 477  
QY 592 GTTCCAGCCTTGTGATATCTGATTTTAACTGGCAAAAGGTGAGGCGATACATA 651  
DB 478 GTAGCCTCGCTGACCAACATCATCTACACACCTCTTTGAGGCGACTGCTGATGATA 537  
QY 652 GCAGATGTCGAACCTTATGAGAGGTGATTTGCTGGAGCCTTATGCTGAAGCATGCT 711  
DB 538 GCAAGCTGTCAAGACGTGGAGAGGTGGCATTTGGGGGTACACAGCATGAGAAAGCCATGCT 597  
QY 712 GGGATATCATCTGTGATTTGCTGCTTTGATCTGCTTATGACGACGAGAAATTTGAC 771  
DB 598 GGGTATACCTTCTGTGGCGCGCGCTGTATCTCTCAAGAGGAAAGCTTCTCTGAC 657  
QY 772 TTGCTTACCTTGTGATTTGCTGCTGCTTTTGTCTCA---AGAGTGAATGCGGATTTCAA 828  
DB 658 TTGAGAGCTTATTTACATGGGTGACAAAGCCGCGCATGCTATTTGAGAGGATTTTCAG 717  
QY 829 GCAGCAATATTAATTTGTTGATGTTGCTACTCTTTTGGCAGC 874  
DB 718 GGCGGCTGCAACAAAGCTGTGATGGCTGCTCTCTTGGCAGC 763

RESULT 12  
AA094413

ID AA094413 standard; cdna: 1248 BP.

AC AA094413:

DT 23-JAN-1996 (first entry)

XX Human farnesyl protein transferase gene beta subunit.

XX Farnesyl transferase; inhibitor; cancer; ras; p21; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1164

FT /tag= a

FT /product= alpha\_farnesyl\_transferase

XX ,US5420245-A.

XX 30-MAY-1995.

XX 18-APR-1990.

XX 16-JAN-1992.

XX 18-APR-1990.

XX 20-NOV-1990.

XX 03-APR-1992.

XX (TEXA ) UNIV TEXAS.

XX Brown MS, Goldstein JL, Rells Y;

XX WPI: 1995-206308/27.

XX P-PDB; AAR7842.

XX New farnesyl transferase inhibitor peptide(s) - based on farnesyl

XX acceptor substrate carboxy terminal sequences, used for the

XX treatment of cancer

XX Example 4; Column 61-62; 55pp; English.

XX AA094413 encodes the beta subunit of human farnesyl transferase

XX which is involved in the farnesylation of various cellular proteins

XX including the cancer related ras proteins. It is used to produce the

XX complete farnesyl transferase molecule which is used to demonstrate

XX the effectiveness of peptide inhibitors capable of inhibiting

CC farnesyl transferases. The peptide inhibitors are useful for  
CC treating cancers and ras-related cancers in particular.  
XX  
SQ Sequence 1248 BP; 286 A; 339 C; 338 G; 285 T; 0 other:

Query Match 14.7%; Score 200.4; DB 16; Length 1248;  
Best Local Similarity 56.2%; Pred. No. 1,9e-51;  
Matches 397; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

QY 172 ATGCTGAGCTGTGGCGCTGATGACATATGACATGACAGGCTGGAGGACATATG 231  
DB 58 AGCTTGTCTTTGAGAGAGGAGAAAGCACTTCTATATCTGAAAAGAGCCCTGCACAACTG 117  
QY 232 GGAACACCTTTCATGATTTAGATGCCAATCGCCCTTGGCTATGCTATGATGCTTCA 291  
DB 118 ACAGATCCCTATGATGCTGTGATGCGACAGCCGCCATGGCTGTGATTTGATGCTGAC 177  
QY 292 CCACCTGCTTTGCTGCTGATGAGCACTTATGATGATCTTGAATGATATATAGACTTC 351  
DB 178 AGCTTGGACCTGCTAGATGAAACCCATCCCCAGATAGTGCTTCAAGATGTGTGATTC 237  
QY 352 TTAGCTGATGTCAGATTAAGATGGTGGATATAGTGTGACCTGGACGCTTGGCTTAC 411  
DB 238 CTGAGCTGTGTGAGAGCCGAGAAAGGTGGCTTTGAGAGAGGACCGGTGATTCACAC 297  
QY 412 CTAGCTAGCATATGCTGCTGCTTAATATACCTTGTGCAATAGGAGCGAAGAGCATTTG 471  
DB 298 CTGGACCCGACATATGAGCAGATGCAATGCTTGTGATGCTTGTGACACCGAGAGGCTAT 357  
QY 472 TCATCATCATATAGGGCAACCTGTACATTTTATGCTGAGATGAAAGATGATACAGT 531  
DB 358 GACATCATTTAAGAGAGGAAAGCTTCTTACATTTTGTACCTCCGTAAGCAACCTGAC 417  
QY 532 GCTTTGAGATGATGATGCTGGCGAATATGATGCTGCTTCTCTACACCGCTATATG 591  
DB 418 TCCCTTCTCATGCTGATGTCGAGGTGAGGTGATGTGAGAAAGCCATATCTGCTGCTC 477  
QY 592 GTTCCAGCCTTGTGATATCTGATTTTAACTGGCAAAAGGTGAGGCGATACATA 651  
DB 478 GTAGCCTCGCTGACCAACATCATCTACACACCTCTTTGAGGCGACTGCTGATGATA 537  
QY 652 GCAGATGTCGAACCTTATGAGAGGTGATTTGCTGGAGCCTTATGCTGAAGCATGCT 711  
DB 538 GCAAGCTGTCAAGACGTGGAGAGGTGGCATTTGGGGGTACACAGCATGAGAAAGCCATGCT 597  
QY 712 GGGATATCATCTGTGATTTGCTGCTTTGATCTGCTTATGACGACGAGAAATTTGAC 771  
DB 598 GGGTATACCTTCTGTGGCGCGCGCTGTATCTCTCAAGAGGAAAGCTTCTCTGAC 657  
QY 772 TTGCTTACCTTGTGATTTGCTGCTGCTTTTGTCTCA---AGAGTGAATGCGGATTTCAA 828  
DB 658 TTGAGAGCTTATTTACATGGGTGACAAAGCCGCGCATGCTATTTGAGAGGATTTTCAG 717  
QY 829 GCAGCAATATTAATTTGTTGATGTTGCTACTCTTTTGGCAGC 874  
DB 718 GGCGGCTGCAACAAAGCTGTGATGGCTGCTCTCTTGGCAGC 763

RESULT 13  
AAT38711

ID AAT38711 standard; cdna: 1248 BP.

AC AAT38711:

DT 30-JUL-1997 (first entry)

XX Human farnesyl transferase enzyme beta subunit cDNA.

XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;

XX ras protein; K-ras B; malignant; detection; identification; ss.

XX Homo sapiens.

XX



```
Db 268 ACAGATGCTACGAGTGTCTGATGCGCCAGCCCATGCTGTCTGATCTTGATCTTGAT 327
Qy 292 CCAGTTCCTTGTGATGAAGCACTTGATGATGATCTTGATGATGATGATGATGATGAT 351
Db 328 AGCTGTGAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 387
Qy 352 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
Db 388 CTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
Qy 412 CTGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
Db 448 CTGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507
Qy 472 TCATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
Db 508 GAGTATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
Qy 532 GCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 591
Db 568 TCTTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627
Qy 592 GTTGGCAGCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
Db 628 GTAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
Qy 652 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
Db 688 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
Qy 712 GGTATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Db 748 GGTATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
Qy 772 TTGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 838
Db 808 TTGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 867
Qy 829 GAGCAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 884
Db 868 GAGCAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 923

RESULT 15
AA064889 standard: cDNA: 2546 BP.
XX
AC AA064889:
XX
DT 07-NOV-1994 (first entry)
XX
DE cDNA encoding human Farnesyl transferase in insert pRO516.
XX
KM Farnesyl protein transferase; Inhibition; farnesylation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 23..1345
FT FT /tag= a
FT FT /note= "alpha subunit"
FT CDS 1348..2487
FT FT /tag= b
FT FT /note= "beta subunit"
XX
PN MO9410184-A.
XX
PD 11-MAY-1994.
XX
PF 29-OCT-1993: 93MO-US10442.
XX
PR 30-OCT-1992: 92US-0968782.
XX
```

```
PA (MER1) MERCK & CO INC.
XX
PI Diehl RE, Gibbs JB, Kohl NE, Omer CA;
XX
DR WPI, 1994-167373/20.
XX
P-PSDB: AAR54832.
XX
PT Mammalian farnesyl protein transferase prodn. - used in assays
XX for cpds. with inhibitory activity for the identification of
XX anticancer agents
XX
PS Disclosure: Fig 5; 69pp; English.
XX
PS The cDNA encoding the human alpha and beta subunits of Farnesyl
XX isolated from a human placental cDNA library in lambda gill using a
XX bovine Farnesyl transferase probe. The Farnesyl transferase can be used to assess the
XX inhibitory activity of a cpd. in the farnesylation of a protein
XX substrate. The assay can be used to identify anticancer agents.
XX See also AA064886-8.
XX
SQ Sequence 2546 BP; 689 A; 607 C; 653 G; 597 T; 0 other:

Query Match 14.5%; Score 197.2; DB 15; Length 2546;
Best Local Similarity 55.9%; Pred. No. 2.9e-50;
Matches 395; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

Qy 172 ATGCTAGAGCTGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 231
Db 230 AGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 289
Qy 232 GAGCAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 291
Db 290 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 349
Qy 292 CCAGTTCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 351
Db 350 AGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 409
Qy 352 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
Db 410 CTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
Qy 412 CTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
Db 470 CTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
Qy 472 TCATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
Db 530 GACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
Qy 532 GCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 591
Db 590 TCTTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
Qy 592 GTTGGCAGCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
Db 650 GTAGCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 709
Qy 652 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
Db 710 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
Qy 712 GGTATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Db 770 GGTATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 829
Qy 772 TTGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
Db 830 TTGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 889
Qy 829 GAGCAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 874
Db 890 GAGCAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 935
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OM nucleic - nucleic search, using sw model

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Searched: 383533 seqs, 122816752 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
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Maximum Match 1008  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	206.6	15.2	2464	1 US-07-863-169A-4	Sequence 4, Appl1
2	206.6	15.2	2464	2 US-08-429-964-4	Sequence 4, Appl1
3	206.6	15.2	2464	3 US-07-935-087-4	Sequence 4, Appl1
4	206.6	15.2	2464	5 PCT-US93-08062-4	Sequence 4, Appl1
5	203.6	15.0	1413	3 US-07-935-087-8	Sequence 8, Appl1
6	202	14.9	1314	1 US-08-424-268-9	Sequence 9, Appl1
7	202	14.9	1314	5 PCT-US93-10442-9	Sequence 9, Appl1
8	200.4	14.7	1248	1 US-07-863-169A-8	Sequence 8, Appl1
9	200.4	14.7	1248	2 US-08-429-964-8	Sequence 8, Appl1
10	200.4	14.7	1248	5 PCT-US93-08062-8	Sequence 8, Appl1
11	199.2	14.7	1314	1 US-08-424-268-5	Sequence 5, Appl1
12	199.2	14.7	1314	7 PCT-US93-10442-5	Sequence 5, Appl1
13	197.2	14.5	2546	1 US-08-424-268-19	Sequence 19, Appl1
14	197.2	14.5	2546	5 PCT-US93-10442-19	Sequence 19, Appl1
15	59	4.3	1306	4 US-09-387-574-3	Sequence 3, Appl1
16	59	4.3	1306	4 US-09-668-096-3	Sequence 3, Appl1
17	49.2	3.6	1330	4 US-09-387-574-5	Sequence 3, Appl1
18	49.2	3.6	1330	4 US-09-668-096-5	Sequence 3, Appl1
19	46.2	3.4	1411	4 US-09-387-574-1	Sequence 1, Appl1
20	46.2	3.4	1411	4 US-09-668-096-1	Sequence 1, Appl1
21	41.2	3.0	1248	4 US-09-105-537-7	Sequence 7, Appl1
22	41.2	3.0	5870	3 US-09-320-878-21	Sequence 21, Appl1
23	41.2	3.0	13613	4 US-09-105-537-3	Sequence 3, Appl1
24	40.6	3.0	1659	4 US-09-083-351-3	Sequence 3, Appl1
25	40.6	3.0	1659	4 US-09-083-352-3	Sequence 3, Appl1
26	40.6	3.0	3946	3 US-09-083-351-1	Sequence 1, Appl1
27	40.6	3.0	3946	4 US-09-083-352-1	Sequence 1, Appl1

28	40.2	3.0	423	1 US-08-470-179-77	Sequence 77, Appl1
29	38.8	2.9	1422	4 US-09-387-574-7	Sequence 7, Appl1
30	38.8	2.9	1422	4 US-09-668-096-7	Sequence 7, Appl1
31	38.6	2.8	1670	1 US-08-189-772-10	Sequence 10, Appl1
32	38.6	2.8	1670	1 US-08-188-277B-5	Sequence 5, Appl1
33	38.6	2.8	1969	1 US-08-188-277B-3	Sequence 3, Appl1
34	38.6	2.8	1969	2 US-08-429-964-79	Sequence 79, Appl1
35	38.6	2.8	2913	1 US-08-188-277B-6	Sequence 6, Appl1
36	38.2	2.8	1187	1 US-08-440-856A-2	Sequence 2, Appl1
37	37.2	2.7	1365	4 US-09-319-892-1	Sequence 1, Appl1
38	36	2.6	1568	1 US-08-188-277B-1	Sequence 1, Appl1
39	36	2.6	1568	2 US-08-429-964-81	Sequence 81, Appl1
40	35.6	2.6	729	1 US-08-189-772-9	Sequence 9, Appl1
41	35.6	2.6	729	1 US-08-188-277B-26	Sequence 26, Appl1
42	35.2	2.6	68750	3 US-09-335-409-1	Sequence 1, Appl1
43	35.2	2.6	68750	4 US-09-568-102-1	Sequence 1, Appl1
44	35.2	2.6	68750	4 US-09-567-969-1	Sequence 1, Appl1
45	35.2	2.6	68750	4 US-09-568-480-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-07-863-169A-4  
; Sequence 4, Application US/07863169A  
; Patent No. 5420245  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Michael S.  
; APPLICANT: Goldstein, Joseph L.  
; TITLE OF INVENTION: Tetrapeptide-Based Inhibitors of Farnesyl  
; NUMBER OF INVENTION: 8  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/863,169A  
; FILING DATE: 03-APR-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/822,011  
; FILING DATE: 19-JAN-1992  
; CLASSIFICATION: 530  
; APPLICATION NUMBER: US 07/937,893  
; FILING DATE: 18-APR-1991  
; CLASSIFICATION: 530  
; APPLICATION NUMBER: US 615,715  
; FILING DATE: 20-NOV-1990  
; CLASSIFICATION: 530  
; APPLICATION NUMBER: US 510,706  
; FILING DATE: 18-APR-1990  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:297/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEEX: 79-0924  
; INFORMATION FOR SEQ. ID NO: 4:  
; SEQUENCE CHARACTERISTICS:



Oy	532	GCCTTCAGAAATGCAATGATGGGCGAAATTGATGCTCCGCTTCTCCACCGCATATCG	591
Db	627	TCCTTTTCATGACGACGTCGCGAGAGAGTGSATTTAAGAACTGCGTACTGCTGCCCTCA	686
Oy	552	GTTCGCCACCCCTTGTGAATATTCCTTGATTTTAACTGSCAAAAGGTGTAGCGCACTACATA	651
Db	687	GTAGCTCTCTCCACCAACATCATCCTCCGACCTCTTCCAGACCACTCGCTGAATGGATA	746
Oy	652	GCAAGATGTCAAACCTTTATGAAAGTGGATTTCTGCGGGAGCCTTATGCTGAAGCAACATGAT	711
Db	747	GCAAGTGCCCAACACTGGGAAGCGCGCATTTGCGGCGGTGCCAGGATGGAAGCCCAAGGT	806
Oy	712	GGGTATACATTTCTGTGATTGGCTGCTTGTGATCCTGTTAATGAGCGAGAAAGTTGAC	771
Db	807	GGCTACACCTTCTGTGGCTTGGCTGGCCCTGGTGTATCCTCAAGAAGCAACGTTCTTGTAC	866
Oy	772	TTGCTATGTTGATTTGGCTGGTGGCTTTTCGTA---AGAGTGAAGTGGGATTTCCAA	828
Db	867	CTGAAGACCTTGCTACATATGGGTACAAGCGCGAGATGGCGTTTCGAAGGAGATTTTCAG	926
Oy	829	GGAGCACTAATAATTGCTTGATGATGGTGTGCTACTTCCTTTTGGCAGGAG	877
Db	927	GGCGCTGCAACCAAGCTGTGTGACGGCGTCTACTTCCTTGTGCGAGGAG	975

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1      RESULT 3
2      US-07-935-087-4
3      ; Sequence 4, Application US/07935087
4      ; Patent No. 6083917
5      ; GENERAL INFORMATION:
6      ; APPLICANT: BROWN, MICHAEL S.
7      ; APPLICANT: GOLDSTEIN, JOSEPH L.
8      ; APPLICANT: REISS, YVVAL
9      ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
10     ; TITLE OF INVENTION: THE IDENTIFICATION,
11     ; TITLE OF INVENTION: CHARACTERIZATION OF,
12     ; TITLE OF INVENTION: AND INHIBITION OF, FARNESYL
13     ; TITLE OF INVENTION: PROTEIN TRANSFERASE
14     ; NUMBER OF SEQUENCES: 8
15     ; CORRESPONDENCE ADDRESS:
16     ; ADDRESSEE: ARNOLD, WHITE & DURKEE
17     ; STREET: P. O. BOX 4433
18     ; CITY: HOUSTON
19     ; STATE: TEXAS
20     ; COUNTRY: USA
21     ; ZIP: 77210
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: FLOPPY DISK
24     ; COMPUTER: IBM PC COMPATIBLE
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: WORDPERCT 5.1 (converted to ASCII-DOS)
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/07/935,087
29     ; FILING DATE: 19920824
30     ; CLASSIFICATION: 435
31     ; PRIORITY APPLICATION DATA:
32     ; APPLICATION NUMBER: US/07/822,011
33     ; FILING DATE: 01/16/92
34     ; ATTORNEY/AGENT INFORMATION:
35     ; NAME: PARKER, DAVID L.
36     ; REGISTRATION NUMBER: 32,165
37     ; REFERENCE/DOCKET NUMBER: UTSD:269/PAR
38     ; TELECOMMUNICATION INFORMATION:
39     ; TELEPHONE: 512-320-7200
40     ; TELEFAX: 512-474-7577
41     ; TELEX:
42     ; INFORMATION FOR SEQ ID NO: 4:
43     ; SEQUENCE CHARACTERISTICS:
44     ; LENGTH: 2464 base pairs
45     ; TYPE: nucleic acid
46     ; STRANDEDNESS: single
47     ; TOPOLOGY: linear

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US-07-935-087-4
Query Match      15.2%;   Score 206.6;   DB 3;   length 2464;
Best Local Similarity 56.7%;   Pred. No. 1.2e-53;
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1

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Qy	172	ATGCTAGAGCGCTGGCGCTGATACACCAATATGAGTATGTGACGGCTGGCGTGAAGGCAATATG	211
Db	267	AGGCTCGTTCTGCAGAGGGAGAACCACTTCATATATCTGAAMAGAGGCGCTTCGACAACTG	326
Qy	232	GGACCAGCCTTTCATGTTCTTATGATGCCAATGCGCCCTGGCTATGCTACTGATGTTCAAT	291
Db	327	ACAAATGCTTATATGAGTGTCTGGAGTCCAGCGCGCCCTGGCTGTCTGTCAATGGAATCCGTGAC	386
Qy	292	CCACTGCTGTTGCGATGTAAGCAACTGTGATGATATCTTACAGAAATGATATCATAGACTTC	351
Db	387	AGCTTTGGAAGCTTCCTCGACGAAGCCATGCCCAATATAGTGGCTACAGATGTGTGTCAATTG	446
Qy	352	TTAGCTGAGTGTGAGATTAAGATGTGATATATGATGTTGGACCTGGACAGTTGCTCAAC	411
Db	447	TTTGAGGCTGTGTCAAGATCCAGACGGTGGCTTTGGAGGGGGCCCTGGTGTCAATCCACACAC	506
Qy	412	CTAGCTACGACTTATNGCTGCTGTAAATATACACTGTGACATATGGAGGCCGAAGACATTG	471
Db	507	CTCGCTCCACAGTATGCAAGCTGTATAAGCGGTATGATCATATGGCACGGAGAAAGCCTTAC	566
Qy	472	TCATCAATCAATTAAGGGCAACCTGTACAAATTTATGCTGCAGATGAAAGATGTATCAGGT	531
Db	567	AACGTCAATTAACAGAGAAACCTCTTCAGTACTGTATCTCCCTAAAGCAACGGATGGC	626
Qy	532	GCTTTACAGATGCATGATGCTGGCGAAATTGATATCCGTGCTCTTCTACACCGCTATATCG	591
Db	627	TCTTTTCTCATGCAACGTCGGGAGGAGGTGATGTAAAGATGCGTACTGTGCTGCTCA	686
Qy	592	GTTGCGACCGCTTGCAATATCTTGATTTTAACTGCGCAAAAGGTGATGAGCGACTACATA	651
Db	687	GTAGCTCTCTCCACCAACATATACCTCTGACCTCTTCGAAAGGCACTGCTGATGATGATA	746
Qy	652	GCAAGATGTCAACTATATGANGTGTATGCTGGGAGCGCTTATGCTGAAGCACATGTT	711
Db	747	GCAAGGTGCCAAGCACTGGGAAGGGCGGATGGCGGGCTCCAGGAGATGAGAAAGCCACGGT	806
Qy	712	GGGTATACATCTGTGGAATGCGTGTGATTCCTGTTATATGAGGCGAGAAAGTTGAC	771
Db	807	GGCTACACCTTCTGTGGCTTGGCTGGCTGGTATCTCTCAAGAAAGAACTGTTCTTGAAC	866
Qy	772	TTGCTTATTTGATTGGCTGGGTGGCTTTTTCGTCA--AGAGTGGAAATCGGAATTTCAA	828
Db	867	CTGAAGACCTTGCTACAAATATGGGTGACAAAGCGCGCAAGATGGGGTTTGAAGAGGATTTTCA	926
Qy	829	GGAGCACTAATAATATGTTGATGATGTTGCTACTCTCTTTTGGCAGGAG	877
Db	927	GGCCGCTGCAACAAGCTGTGGTGAAGGGCTGTACCTCTTGTGGAGGAG	975

RESULT 4-08062-4  
PCT-US93-08062-4  
Sequence 4 Application PC/TUS9308062  
GENERAL INFORMATION:  
APPLICANT:  
SEQUENCE CHARACTERISTICS:  
SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.  
SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.  
SEQUENCE CHARACTERISTICS: REISS, YUVAL  
SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.  
ADDRESSEE: METHODS AND COMPOSITIONS FOR  
ADDRESSEE: THE IDENTIFICATION  
ADDRESSEE: CHARACTERIZATION AND  
ADDRESSEE: INHIBITION OF  
ADDRESSEE: FARNESYLTRANSFERASE  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DUREKE

STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK/ASKII  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08062  
FILING DATE: AUGUST 24, 1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/935,087  
FILING DATE: 24 AUGUST 1992 (24.08.92)  
NAME: UNKNOWN  
ATTORNEY/AGENT INFORMATION:  
NAME: PARKER, DAVID L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTP377PCT  
TELEPHONE: 512-320-7200  
TELEFAX: 512-474-7577  
TELEX: NOT APPLICABLE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2464 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US93-08062-4

Query Match 15.2% Score 206.6; DB 5; Length 2464;  
Best Local Similarity 56.7%; Pred. No. 1.2e-53;  
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGCTGATGACATATCTGACGCGCTGGCTGAGGACATATG 231  
DB 267 AGGCTGCTTGTGACAGAGGAAAGCACTTCATATCTGAAGAAGCGCTTCGACACTG 326  
QY 232 GGACCAAGCTTTCATGTTCTAGATGCCAATGCCCTTGGCTATGCTAGTGGATTCAT 291  
DB 327 ACAGATCCCTATGATGCTGAGCCAGCCGCCCTGGCTGCTGATGATCTGCTGAC 386  
QY 292 CCACTTCCTTGGCTGATGAGCACTGATGATGATGATGATGATGATGATGATGATG 351  
DB 387 AGCTTGAGCTCTCGACGAACCATCCCAATAGTGCCTACAGATGCTGCTGCTGCTG 446  
QY 352 TTAGCTGATGCTGAGATTAAGATGATGATGATGATGATGATGATGATGATGATG 411  
DB 447 TTGGAGCTGTGCTGAGATCCAGAGGCTGGCTTGGAGGGGCGCTGCTGATGCTGCTG 506  
QY 412 CTAGCTAGCACTATGCTGCTGTAATACACTTGTGACATAGGAGCGAAGAGCTTG 471  
DB 507 CTGCTGCCAGATGATGCTGTAACAGCGCTATGATGATGATGATGATGATGATGATG 566  
QY 472 TCATCATCATATAGGCGCACTGTACATTTTATGCTGAGATGAAGAATGATACG 531  
DB 567 AACGTCTATTAACAGAGAAAGCTCTTCACTACTTGTACTTCCCTAAAGCAACCGGATG 626  
QY 532 GCTTTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
DB 627 TCTTTCTGCTGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 686  
QY 592 GTTCCAGCACTTGTGATATTTCTTGAATTTAAATGCGCAAAAGCTGTAGCGCATAC 651  
DB 687 GTAGCCCTCTGCAACAATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 746  
QY 652 GCAAGATGCTCAAACTTATGAAAGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 711  
DB 747 GCAAGGTGCAAACTGAGAGAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806

QY 712 GCGTATACATCTGTGGATGCTGCTTGTGATCCTGTTAATGAGCAGAAAGTTGAC 771  
DB 807 GCGTACACCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 866  
QY 772 TTGCTAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828  
DB 867 CTGAAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 926  
QY 829 GGAAGCACTAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 877  
DB 927 GGGCGCTGCAACAAGCTGTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 975

## RESULT 5

US-07-935-087-8  
Sequence 8, Application US/07935087  
Patent No. 6083917  
GENERAL INFORMATION:  
APPLICANT: BROWN, MICHAEL S.  
APPLICANT: GOLDSTEIN, JOSEPH L.  
APPLICANT: REISS, YUVAL  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TITLE OF INVENTION: THE IDENTIFICATION,  
TITLE OF INVENTION: CHARACTERIZATION,  
TITLE OF INVENTION: AND INHIBITION OF FARNESYL  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURREE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,087  
FILING DATE: 19920824  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/822,011  
FILING DATE: 01/16/92

ATTORNEY/AGENT INFORMATION:  
NAME: PARKER, DAVID L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:269/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-320-7200  
TELEFAX: 512-474-7577  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1413 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-935-087-8

Query Match 15.0% Score 203.6; DB 3; Length 1413;  
Best Local Similarity 56.5%; Pred. No. 7.1e-53;  
Matches 399; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGCTGATGACATATCTGACGCGCTGGCTGAGGACATATG 231  
DB 265 AGGCTGCTTGTGACAGAGGAAAGCACTTCATATCTGAAAAGAGCGCTTCGACAACTG 324  
QY 232 GGACCAAGCTTTCATGTTCTAGATGCCAATGCCCTTGGCTATGCTACTGATGATTCAT 291

Db 325 ACAGATGCTATGAGTGTCTGATGCGACGCCCATGGCTCTGTAATTGGATCCTGAC 384  
Oy 292 CCAGTTCCTTTGGCTGATGAAGCACTTGATGATCTTGAGATGATATCATAGACTTC 351  
Db 385 AGCTTGAACTGCTAGATGATCCATCCCATGATAGTGTGCTACAGATGTGTGACGTTG 444  
Oy 352 TTGAGCTCGATGTGAGATGAAGTGGTGGATATAGTGTGAGTGTGAGTGTGAGTGTG 411  
Db 445 TTGGAGCTGTGTGAGCCGAGAGAGTGGCTTTGGAGGAGGACCGCTGATTCACAC 504  
Oy 412 CTAGCTACGACTTATGCTGTGAATACACTTGTGACATAGGAGGAGGAGGAGTGTG 471  
Db 505 CTGGACACCCATATGACAGAGTCAATGATGATGATGATGATGATGATGATGATGATG 564  
Oy 472 TCATCAATCAATAGGGGCAACTGTACAAATTTATGCTGACATGAAGAATGATCAGT 531  
Db 565 GACATGATTAACAGAGAGAGCTTTCAGATTTTGTACTCCCTGAAGCAACTGACGCG 624  
Oy 532 GCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
Db 625 TCTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684  
Oy 592 GTTCCAGCCTTGTGATATTTCTGATTTTAACTGGCAAAAGTGTAGGCACTACATA 651  
Db 685 GTAGCCTCGCTGACCAACATCATCATCCAGACTCTTTAGAGGCACTGCTGATGATA 744  
Oy 652 GCAAGATGCAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711  
Db 745 GCAAGGCTGACAACTGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 804  
Oy 712 GGTATACATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771  
Db 805 GGTATACATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 864  
Oy 772 TTCCCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 828  
Db 865 TTGAGAGCTTATTAATATGATGATGATGATGATGATGATGATGATGATGATGATG 924  
Oy 829 GAGCAACTATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 874  
Db 925 GGCCGCTGCAACAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 970

RESULT 6  
US-08-424-268-9  
; Sequence 9, Application US/08424268  
; Patent No. 582118  
; GENERAL INFORMATION:  
; APPLICANT: Omer, Charles A  
; APPLICANT: Diehl, Ronald E  
; APPLICANT: Glibbs, Jackson B  
; APPLICANT: Kohl, Nancy E  
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: United States of America  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: System 7.5.3  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,268  
; FILING DATE: 4/24/95  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muthard, David A

; REGISTRATION NUMBER: 35,297  
; REFERENCE/DOCKET NUMBER: 18858PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-3903  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ. ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1314 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; US-08-424-268-9

Query Match 14.9%; Score 202; DB 1; Length 1314;  
Best local similarity 56.4%; Pred. No. 2, le-52;  
Matches 398; Conservative 0; Mismatches 305; Indels 3; Gaps 1;

Oy 172 ATGCTAGAGCTGTGCGCTGATCAGCATATGAGATCTGACGCGCTGAGGCAATATG 231  
Db 208 AGGCTTGTGTCAGAGAGGAGGAGCACTTCATATCTGAAGAGGCTTCGACAACTG 267  
Oy 232 GACACAGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 291  
Db 268 ACAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 327  
Oy 292 CCAGTTCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 351  
Db 328 AGCTTGAACTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 387  
Oy 352 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411  
Db 388 CTGAGAGCTGTGACAGCCAGAGAGTGGCTTTGAGAGGAGCCGGTCAATATCCAC 447  
Oy 412 CTAGCTACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 471  
Db 448 CTGAGCCACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507  
Oy 472 TCATCAATCAATAGGGGCACTGTACATTTTATGCTGCAAGTGAAGATGATCAGT 531  
Db 508 GACATCATTTAACAAGAGAAAGCTTCTACATATTTGTACTCCCTGAAGCAACTGAC 567  
Oy 532 GCTTTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
Db 568 TCTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627  
Oy 592 GTTCCAGCCTTGTGATATTTGATTTTAACTGGCAAAAGTGTAGGCACTACATA 651  
Db 628 GTAGCCTCGCTGACCAACATCATCATCCAGACCTCTTTAGAGGCACTGCTGAATG 687  
Oy 652 GCAAGATGCAAACTTGAAGAGTGTATGCTGGGAGGCTTATGCTGAAGCAATGAT 711  
Db 688 GCAAGGTGTGAGACTGGAAGTGTGATGCTGGGATGACAGGATGAGAGGCACTGAT 747  
Oy 712 GGTATACATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 771  
Db 748 GCGATATCTTGTGCTGTGCGCGCGCTGTATCTCTCAAGAGGCAACTTCTTGAAC 807  
Oy 772 TTGCTAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 828  
Db 808 TTGAGAGCTTATTAATATGATGATGATGATGATGATGATGATGATGATGATGATG 867  
Oy 829 GAGCAACTATTAATATGATGATGATGATGATGATGATGATGATGATGATGATG 874  
Db 868 GGCCGCTGCAACAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 913

RESULT 7  
PCT-US93-10442-9  
; Sequence 9, Application PC/TUS9310442  
; GENERAL INFORMATION:





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QY 532 GCTTTCAGATGATGATGGGAAATGATGCTCCCTTCTACACCGCTATATGC 591
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 TCCTTCTCATGATGATGGAGGATGAGTGTGATGAGGAGCGATCTGCTGCCCTCC 477
QY 592 GTTCCAGCCCTTGTGAATATCTTGTATTTAACTGGCAAAAGGTGACCGACTACATA 651
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 GTAGCCCTCGGTGACCAATCATCATCTACACAGACCTTTTGAAGGCACTGCTGATGATGA 537
QY 652 GCAAGATGTCAAACTTATGAGAGGTGATGCTGGGAGGCTTATGCTGAAGCAGATGCT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 GCAAGGTGTCAAGACTGGAAGGTGGATGCGGGGTACCAAGGATGGAAGCCCATGCT 597
QY 712 GCGTATACATCTGTGTGATGCTGCTTTGATCCCTGCTTAATGAGCCAGAAAGTTGAC 771
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 GCGTATACCTTGTGTGCTGCGCGCGCTGTATCTCTCAAGAGGAAAGCTTCTTGAC 657
QY 772 TTGCTAGTTGATGGCTGGGTGGCTTTTCGTCA---AGAGTGGAAATGCGATTGCA 828
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 TTGAAGGCTTATTACATATGGGTGACAAAGCCGCGAGATGCTATTGGAAGAGATTTCAG 717
QY 829 GGAAGCACTAATAATGTTGTTGATGCTTCTACTCTTTTGGCAG 874
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 718 GGCGGCTGCAACAAGCTGGTGGATGCTGCTACTCTTCTTGCGCAG 763

RESULT 10
PCT-US93-08062-8
; Sequence 8, Application PC/TUS9308062
; GENERAL INFORMATION:
; APPLICANT:
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
; SEQUENCE CHARACTERISTICS: REISS, YUVAL
; SEQUENCE CHARACTERISTICS: MASTERS, JR., JAMES C.
; ADDRESSEE: METHODS AND COMPOSITIONS FOR
; ADDRESSEE: THE IDENTIFICATION,
; ADDRESSEE: CHARACTERIZATION AND
; ADDRESSEE: INHIBITION OF
; ADDRESSEE: FARNESYLTRANSFERASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08062
; FILING DATE: AUGUST 24, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/935,087
; FILING DATE: 24 AUGUST 1992 (24.08.92)
; NAME: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTPF377PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1248 nucleic acids

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-08062-8
Query Match 14.7%; Score 200.4; DB 5; Length 1248;
Best Local Similarity 56.2%; Pred. No. 6,4e-52;
Matches 397; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

QY 172 ATGCTGAGCTGTGGGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 231
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 AGCTTTGTTTGGCAGAGGGAAGCACTTCTATATCTGAAAAGAGCCCTTGACAACTAG 117
QY 232 GGAACAGCCCTTTCATGCTGTAGATGCCATCGCCCTTGTATGCTACTGATGATGATGATG 291
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 ACAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 177
QY 292 CCACCTTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 351
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 AGCTTGGAACTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 237
QY 352 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 CTGAGAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 297
QY 412 CTAGCTAGCACTTATGCTGCTGTAATACACTTGTGATGATGATGATGATGATGATGATG 471
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 CTGACACCCACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 357
QY 472 TCATCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 531
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 GACATATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
QY 532 GCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 TCCTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
QY 592 GTTCCAGCCCTTGTGAATATCTTGTATTTAACTGGCAAAAGGTGACCGACTACATA 651
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 GTAGCCCTCGGTGACCAATCATCATCTACACAGACCTTTTGAAGGCACTGCTGATGATGA 537
QY 652 GCAAGATGTCAAACTTATGAGAGGTGATGCTGGGAGGCTTATGCTGAAGCAGATGCT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 GCAAGGTGTCAAGACTGGAAGGTGGATGCGGGGTACCAAGGATGGAAGCCCATGCT 597
QY 712 GCGTATACATCTGTGTGATGCTGCTTTGATCCCTGCTTAATGAGCCAGAGAAAGTTGAC 771
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 GCGTATACCTTGTGTGCTGCGCGCGCTGTATCTCTCAAGAGGAGACTTCTTGAAAC 657
QY 772 TTGCTAGTTGATGGCTGGGTGGCTTTTCGTCA---AGAGTGGAAATGCGATTGCA 828
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 TTGAAGGCTTATTACATATGGGTGACAAAGCCGCGAGATGCTATTGGAAGAGATTTCAG 717
QY 829 GGAAGCACTAATAATGTTGTTGATGCTTCTACTCTTTTGGCAG 874
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 718 GGCGGCTGCAACAAGCTGGTGGATGCTGCTACTCTTCTTGCGCAG 763

RESULT 11
US-08-424-268-5
; Sequence 5, Application US/08424268
; GENERAL INFORMATION:
; APPLICANT: Omer, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; TITLE OF INVENTION: Transferase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000

```



CITY: Rahway  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Power Mac  
OPERATING SYSTEM: System 7.5.3  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,268  
FILING DATE: 4/24/95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mulhard, David A  
REGISTRATION NUMBER: 35,297  
REFERENCE/DOCKET NUMBER: 18858PC  
TELEPHONE: (908) 594-3903  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1314 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-424-268-5

Query Match 14.7% Score 199.2; DB 1; Length 1314;  
Best Local Similarity 55.9%; Pred. No. 1.5e-51;  
Matches 400; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGGCTATCGCATCGATCTGACCGCTGGCTGAGGCGATATG 231  
DB 208 AGGCTGTGTTTGGAGAGAGGACATTCATATCTGAAAAGAGCGCTCCGACAGCTG 267  
QY 232 GGACCAAGCTTTTCATGTTAGATGCAATGCGCTTGGCTATGCTAGTGGATTGAT 291  
DB 268 ACAGATGCTAGAGAGTGTGATGTCAGCGCCCATGGCTCTGCTAGTGGATCTGAT 327  
QY 292 CCACCTGCTTGTGATGATGACGATTTGATGATCTTGAGATATATATGACATTC 351  
DB 328 AGCTGGAATCTCTGATGAGCCATCCCCAAGATGCTGCGCACAGCTGTCTAGTTC 387  
QY 352 TTAGCTGATGTCAGATTAAGATGATGATGATGATGATGATGATGATGATGATG 411  
DB 388 CTGGAGTTGTGAGAGCCAGAGAGCGGCTTGGAGGGGCGCTGCGCAGTACCCAC 447  
QY 412 CTAGCTAGCACTTATGCTGCTGTAATACACTGTGACATATAGGAGCAAGACATTC 471  
DB 448 CTGGACCAAGCATGACAGGGGTCAACGGCTGTGCATCATTTGGACCGAGAGCGCT 507  
QY 472 TCATCATCATATGAGGCAACTGTACATTTTATGCTGCAATGAAAGATGATAGGT 531  
DB 508 GAGCTGATTAACAGAGAGAGGCTTCTCAGTATTTACTCGCTGAAGCAACCCGAT 567  
QY 532 GCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
DB 568 TCTTTTCTCATGACATGAGTGTGAGTGTGAGAGTGAAGTCAATCTGCTGCTGCT 627  
QY 592 GTTGCCAGGCTGTGATATTTCTGATTTTAACTGCAAAAGCTGTAGCGCACTAT 651  
DB 628 GTAGCTTGTGACCAACATCATCACCGACCTGTTTGAAGGCACTGTGATGATG 687  
QY 652 GCAGATGTCAAACTATGAGGTGTATTTGCTGGGAGCGCTTATGCTGAGCAATG 711  
DB 688 GCAAGGTGTGATGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 747  
QY 712 GGGTATACATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 771

DB 748 GGCTACACGTTCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTG 807  
QY 772 TTGCTAGTTGATTTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTG 828  
DB 808 TTGAGAGCTTACTACATGAGTGTGACAGCGGCAATGATGATGATGATGATGAT 867  
QY 829 GCAGCACTAATAATTTGTTGATGTTGCTGCTACTCTTTTGGCAGGAGCTGCC 884  
DB 868 GGCGCTGCAACAGCTGTGAGAGCGCTGTCTACTCTTCTGCGAGCGGCTGCT 923

RESULT 12  
PCT-US93-10442-5  
Sequence 5, Application PC/TUS9310442  
GENERAL INFORMATION:  
APPLICANT: Omer, Charles A  
APPLICANT: Diehl, Ronald E  
APPLICANT: Gibbs, Jackson B  
APPLICANT: Kohl, Nancy E  
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10442  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/968,782  
FILING DATE: 10/30/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mulhard, David A  
REGISTRATION NUMBER: 35,297  
REFERENCE/DOCKET NUMBER: 18858  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3903  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1314 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US93-10442-5

Query Match 14.7% Score 199.2; DB 5; Length 1314;  
Best Local Similarity 55.9%; Pred. No. 1.5e-51;  
Matches 400; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGCTGATTCAGATATCGATCTGACCGCTGGCTGAGGCAATG 231  
DB 208 AGGCTGTGTTTGGAGAGAGGACATTCATATCTGAAAAGAGCGCTCCGACAGCTG 267  
QY 232 GGACCAAGCTTTTCATGTTAGATGCAATGCGCTTGGCTATGCTAGTGGATTGAT 291  
DB 268 ACAGATGCTAGAGAGTGTGATGTCAGCGCCCATGGCTCTGCTAGTGGATCTGAT 327  
QY 292 CCACCTGCTTGTGATGATGACGATTTGATGATCTTGAGATATATATGACATTC 351  
DB 328 AGCTGGAATCTCTGATGAGCCATCCCCAAGATGCTGCGCACAGCTGTCTAGTTC 387

Oy	352	TTAGCTGATGTGACGAGTAAGAAGATGATGGATATATAGTGTGTGACCTGTGACAGAGTTGCCAC	4111
Db	388	CTGAGAGTTGTGTACAGACCCCAAGAAAGCCGCTTTTGGAGGGGGCCCTGTGGCCACGTACCACAC	4477
Oy	412	CTAGCTAGCACTTATGCTGTGTAAATACACTTGTGCAMTATGGAGCCGAAGAGCATTG	4711
Db	448	CTTGGCACCAGTATGTCAGCGGTCAACGCCCTGTGCATCATTTGGCACCCGAGAGGCTTAT	5077
Oy	472	TCATCAATCANTAGGGGGAACCTGTACAAATTTATGCTGCAGATGGAAGAATGTATCAGT	5311
Db	508	GACGTCATTTAACAGAGAGACCTTCTCCAGATTTGTACTGTGTGAAGCAACCCGATGCG	5677
Oy	532	GCTTTCAGAAATGCATGATGCTGGGGAAATTGATGTCCGTCTTCTACACCGCATATCG	5911
Db	568	TCTTTCTCATGACAGATGAGAGGTAGGTGACGTGGAAGATGCATCTGCTGCTGCTCG	6277
Oy	592	GTTGCGACCCTTGTAATATCTTGATTTTAACTGGCAAAAGGTGTAGGCGACTACATA	6511
Db	628	GTAGCTTGCTGTACCAACATCATACCCACAGACCTGTTTGGGGCCACTGCTGTGAATGTATC	6877
Oy	652	GCAAGATGTCAAACTTATGAAAGGTGTATTTGCTGGGGAGCCTTATGCTGAAGCAGCATGT	7111
Db	688	GCAAGGTCTCAGAAATTTGGGAAGTGTGGATTTGGGGGGTACACAGGAATGGAAGGCCATGGC	7477
Oy	712	GGGTATACATTTCTGTGGATTTGGCTTGTATCTCTGTTAATAGGCCAGAAAGTTGAC	7711
Db	748	GGCTACAGCTTCTGTGGCTGTGGCTGTGGCTGTGCTCATCTCAAGAAAGAGCGCCTCTTGAC	8077
Oy	772	TTGCTTACTTTGATTTGGCTGTGGCTGTGGCTTTTGCTGA---AGAGTGCAGATCGGATTTGCA	8288
Db	808	TTGAAGACCTTACTACATTTGGGTGTACAAAGCCGACAGATGAGCTTTGAAGGTGCATTTGAG	8667
Oy	828	GGACCACTAATAATTTGGTGTGATGTGCTTACTTCTTTTGGCAGGAGCACTGCCAT	8844
Db	868	GGCCCTCTCAACACAGCTGTGTAGAGGGCTGTACTCTTGTGGCAGCGGGCTTCTCT	9223

RESULT 13  
 ; Sequence 19, Application US/08424268  
 ; Patent No. 5821118  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Omer, Charles A  
 ; APPLICANT: Diehl, Ronald E  
 ; APPLICANT: Glibbs, Jackson B  
 ; APPLICANT: Kohl, Nancy E  
 ; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein  
 ; TITLE OF INVENTION: Transferase  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O.Box 2000  
 ; CITY: Rahway  
 ; STATE: New Jersey  
 ; COUNTRY: United States of America  
 ; ZIP: 07065-0907  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Power Mac  
 ; OPERATING SYSTEM: System 7.5.3  
 ; SOFTWARE: Microsoft Word 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/424,268  
 ; FILING DATE: 4/24/95  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mulhard, David A  
 ; REGISTRATION NUMBER: 35,297  
 ; REFERENCE/DOCKET NUMBER: 18858PC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908)594-3803  
 ; TELEFAX: (908) 594-4720

```

: INFORMATION FOR SEQ ID NO: 19:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 2546 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA
:
: HYPOTHEetical: NO
:
: ANTI-SENSE: NO
:
US-08-424-266-19

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Query Match	14.5%	Score 197.2;	DB 1;	Length 2546;
Best Local Similarity	55.9%	Pred. No. 9.7e-51;		
Matches 395; Conservative	0;	Mismatches 308;	Indels 3;	Gaps 1;

OY	172	ATCTGAGAGCGTGGCCGATACACATATCGATATCTGACGCCCTGGGCGTAGGCATATG	231
Db	230	AGGCTGTTTGTTCAGAGGGAGACAGCATCTTCATTTATCTGAAAAGAGCCCTTCGCAACATG	289
OY	232	GGACAGCCCTTTCATGTTCTCTAGATGCCAATGCCCTTGGCTATGCTACTGGATGGTTCAT	291
Db	290	ACAGATGCCCTATGATGCTGTGGATGGAGCGGCCCATGGCTCTGCTATTGGATCCTGCAC	349
OY	232	CCACTTGGCTTTCCTGGATGCAAGCACCTTGATATATATCTTGAGAAATGATATCATAGACTTC	351
Db	350	AGCTTGGAACTGCTAGATGAACCCATCCGCCAGATAGTGGCTACAGATGTGTGCTCACTTC	409
OY	352	TTAGCTGCATCTCAGAGATAAGATATGCTGGATATATAGTGTGGACCTCGACATGCCCTCAC	411
Db	410	CTGGAGCTGTGTCAAGAGCCAGAAAGGTGGCTTTGGAGAGAGACCGGGTCAGTATCCACAC	469
OY	412	CTAGCTACGACTTATGCTGCTGTCTAAATATCACTTTGTACAAATAGGAGACGAAGAAGCTTG	471
Db	470	CTTGGACCCACATATATGACGAGCATATGCAATTTGTCATCTATGGCACCGAGAGGCCCTAT	529
OY	472	TCATCATCATATAGGGGACACCTGTACAAATTTATGCTGCAGATGAAGAAGATGTATCAGT	531
Db	530	GACATCATTTAACAGAGAAAGACCTTCTCAGTATTTGTATCTCCCTGAAAGCACTGCAGCGC	589
OY	532	GCTTTCAGATATGATGATGTGGCGAAATGTATGCTCCGTCTCTACACCGCTATATYC	591
Db	590	TCCCTTTCATGACATGTGGGAGGTGAGCTGTGATGGAAGCCGATACGTGTGCTGCTCC	649
OY	592	GTTGGACACCTTGTGAATATCTTGATTTTAACTGGCAGAAAGGTGAGGGCACTACATA	651
Db	650	GTAGCTGCTGTCACACATATCATCTCAGACCTCTTTGAGGCCACTGCTGCAATGSAITA	709
OY	652	GCAAGATGTCAAACTTATGAAGGTGTATTGCTGGGGAGCCCTTATGCTGAAGCAGCATGT	711
Db	710	GCAMGTCTCAGAACTGGGAAGTGGGACTTTGGCGGGGACAGGAGATGGAAGCCCATGGT	769
OY	712	GGGTATACATTCCTGTGGATTTGGCTGCTTTTGAATCCTGCTATATAGGCAAGAAAGTTGAC	771
Db	770	GGCTATACCTCTGTGGCTGTGGCGCGCTGGTATATCTCAAGAGGAGAACTTCCCTGTAAC	829
OY	772	TTGCTTACTTGTATGGCTGGGTGGCTTTTGTA--AGAGTGAAGATCGGATTTTCAA	828
Db	830	TTGAAGACCTTATTCATCATGGGTGACAAAGCGGACAGATGGCATTTTGAAGGAGGATTTACG	889
OY	828	GGAGCACTAATAATTGGTGTGATGTGCTTACTTCCTTTTGGCAGG	874
Db	890	GCGCGTCTCAACAGCTGTGGTGAATGGCGTCACTTCCTTCTGGAGG	935

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RESULT 14
PCT-US93-10442-19
: Sequence 19, Application PC/TUS9310442
:
: GENERAL INFORMATION:
:
: APPLICANT: Omer, Charles A
:
: APPLICANT: Diehl, Ronald E
:
: APPLICANT: Gibbs, Jackson B
:
: APPLICANT: Kohl, Nancy E
:
: TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-protein

```

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; TITLE OF INVENTION:  Transferrase
; NUMBER OF SEQUENCES:  22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Merck & Co., Inc.
; STREET:  P.O. Box 2000
; CITY:  Rahway
; STATE:  New Jersey
; COUNTRY:  United States of America
; ZIP:  07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; OPERATING SYSTEM:  IBM PC compatible
; SOFTWARE:  Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  PCT/US93/10442
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:  07/968,782
; FILING DATE:  10/30/92
; ATTORNEY/AGENT INFORMATION:
; NAME:  Mulhard, David A
; REGISTRATION NUMBER:  35,297
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (908) 594-3903
; TELEFAX:  (908) 594-4720
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2546 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  cDNA
; HYPOTHETICAL:  NO
; ANTI-SENSE:  NO
; PCT-US93-10442-19

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Query Match 14.5%; Score 197.2; DB 5; Length 2546;

Best Local Similarity 55.9%; Pred. No. 9.7e-51;

Matches 395; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

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QY 172 ATCTGAGCTGTGGGCTGATGACATATGACATATCTGACGCTGGCGCTGAGGCATATG 231
DB 230 AGCGCTGTTTGGAGAGGAGGAGCACTTCATATCTGAAAAGGCGCTTCGACAACTG 289
QY 232 GGACGACCTTTGATGCTGTAGATGCAATGCGCTTGGCTATGCTAGTGGATGTTTCA 291
DB 290 ACAGATGCGTATGATGATGCTGATCGAGCGGCCCATGCTCTCTATTGATGCTGAC 349
QY 292 CCATTCGCTTGTGATGATGACGACCTTGTATGATGATCTTGAAGATGATATGACCTTC 351
DB 350 AGCTTGAACTGCTAGATGAAACCATCCCAATGATGCTGACATGATGCTGCTCACTG 409
QY 352 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
DB 410 CTGAGCTGTGTAGAGCCGAGAGGCTGTTGGAGAGAGCGCGCTGATGATGATGATGAT 469
QY 412 CTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
DB 470 CTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
QY 472 TCATCAATCAATAGGGGCAACTGTACAAATTTTATGCTGAGATGAAAGATGATCAGGT 531
DB 530 GACATCAATTAACAGAGAGAGCTTCTTCACTATTTTATGCTGAGAGCAACTGAGAGG 589
QY 532 GCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 591
DB 590 TCCCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
QY 592 GTTGCAGCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
DB 650 GTAGCTCGCTGACAAACATCATCTCCAGACCTCTTTGAGGGGCTGCTGATGATGATA 709

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QY 652 GCAAGATGTCMAACTTATGAGGTGATGCTGGGAGCCTTATGCTGAGACATAGT 711
DB 710 GCAAGGTGTCMAAAGTGGAGAGGCGCATTTGGCGGGTACGAGGATGCAAGCCCATG 769
QY 712 GGGTATACATCTTGTGATGCTGCTTTGATCTCTGTTATATGACGAGAAAGTTGAC 771
DB 770 GGGTATACCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
QY 772 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 838
DB 830 TTGAGAGCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 889
QY 829 GGAAGCACTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 874
DB 890 GGGCGCTGCAACAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 935

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RESULT 15

US-09-387-574-3

Sequence 3, Application US/09387574

Patent No. 6168951

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Kinney, Tony

APPLICANT: Rafalski, Antoni

TITLE OF INVENTION: Plant Geranylgeranyl Transferrases

FILE REFERENCE: BB-1239

CURRENT FILING DATE: 1999-08-31

EARLIER APPLICATION NUMBER: 60/098,743

EARLIER FILING DATE: September 1, 1998

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Microsoft Office 97

SEQ ID NO 3

LENGTH: 1306

TYPE: DNA

ORGANISM: Glycine max

US-09-387-574-3

Query Match 4.3%; Score 59; DB 4; Length 1306;

Best Local Similarity 45.7%; Pred. No. 3.4e-08;

Matches 206; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

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QY 478 ATCAATAGGGGCAACTGTACAAATTTTATGCTGCAGATGAAGATGATCAGGTCTTC 537
DB 409 ATTGATATGATTAAGGTCACAAAGTTATATGCTGACCTGCAAAATGAAGATGATCCTT 468
QY 538 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
DB 469 TCAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
QY 598 AGCTTGTGATTAATTTTATGATTTTAACTGCAAAAGGTGATGAGCTGATGACAGA 657
DB 529 TCATATATTAATGCTGCTTGTGATTAATATGATGATGATGATGATGATGATGATGAT 588
QY 658 TGTCAAACTTATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
DB 589 TGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
QY 718 ACATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
DB 649 ATTTTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
QY 778 AGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
DB 709 CTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
QY 838 AATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
DB 769 GAGAATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
QY 898 AAGTTAATTAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 928

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Db 829 AGGTACATTGGATTAGTAAGGAGACCTTA 859

Search completed: November 1, 2002, 15:40:38  
Job time : 60 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 12:41:54 ; Search time 1796 Seconds

(without alignments)  
10212.896 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359  
Sequence: 1 atgagcccccctccgcagtc.....agttctctcagaagatga 1359

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estbta:\*  
2: em\_estchm:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	328.6	24.2	675	9	AL506683
3	309.2	22.8	715	9	BE214204
4	306	22.5	694	10	BF634888
5	295	21.7	731	10	BG600901
6	275.4	20.3	582	9	BE194182
7	254	18.7	639	9	AL509620
8	248	18.2	639	10	BG095687
9	242	17.8	521	9	BE129712
10	232	17.1	533	9	AM120078
11	225.8	16.6	506	10	BM177970
12	215.6	15.9	488	10	BF097538
13	211.8	15.6	457	9	AI488509
14	202	14.9	2707	11	BC013574
15	188	13.8	553	9	AM508684
16	182.8	13.5	579	9	BE022297
17	179.6	13.2	541	9	AL510109

18	160.6	11.8	796	9	AU135633
19	159.8	11.8	671	9	AL586940
20	156.8	11.5	937	10	BG325222
21	155.2	11.4	417	10	BM172851
22	154.2	11.3	841	10	BG761213
23	144.8	10.7	600	10	BG801722
24	143.6	10.6	636	9	AL638378
25	143	10.5	771	10	BF162476
26	142.6	10.5	778	9	AI151779
27	142	10.4	511	10	BJ187628
28	138.2	10.2	469	9	AM596366
29	137.6	10.1	690	10	BI335119
30	136.2	10.0	856	10	BI246235
31	134.2	9.9	1604	10	BG257205
32	132.2	9.7	748	10	BI520188
33	132.2	9.7	759	10	BI755078
34	131	9.6	429	10	BI424834
35	131	9.6	589	10	BE824252
36	129.2	9.5	632	10	BM488977
37	128	9.4	314	10	BE398203
38	122.2	9.0	774	10	BG731877
39	121.2	8.9	235	9	AM683980
40	119.2	8.8	623	10	BJ111625
41	118.8	8.7	741	10	BG128793
42	118.8	8.7	1004	10	BG761267
43	118.4	8.7	697	10	BM407893
44	117.8	8.7	710	10	BI178887
45	115.8	8.5	598	10	BI516491

#### ALIGNMENTS

RESULT 1  
BG594738 794 bp mRNA linear EST 12-APR-2001  
LOCUS EST493416 CSTS Solanum tuberosum CDNA clone CSTS866 5' sequence,  
DEFINITION mRNA sequence.  
ACCESSION BG594738.1 GI:13612878  
VERSION  
KEYWORDS  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 794)  
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,  
Bouari,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.  
Unpublished (2000)  
TITLE Contact: Cathy Ronning  
JOURNAL  
COMMENT The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: M13F-R.  
Location/Qualifiers  
1..794  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="CSTS866"  
/clone\_1lb="CSTS"  
/tissue\_type="sprouting eyes from tubers"  
/dev\_stage="12-14 weeks post harvest"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were  
taken from tubers. The tubers were incubated at 26C in the  
dark for 2-3 weeks prior to sprouting. The eyes were  
frozen in liquid nitrogen immediately upon removal from  
tubers."

#### FEATURES

source

BASE COUNT

208 a 149 c 206 g 231 t



RESULT 3	715 bp	MRNA	linear	EST 23-OCT-2001
BE214204				
LOCUS				
DEFINITION	BE214204			
ACCESSION	BE214204			
VERSION	BE214204.3			
KEYWORDS	EST.			
SOURCE	Barley.			
ORGANISM	Hordeum vulgare			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae; Triticeae; Hordeum.			
AUTHORS	1 (bases 1 to 715)			
TITLE	Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.			
JOURNAL	Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library			
COMMENT	Unpublished (2001) On Jul 3, 2000 this sequence version replaced gi:13263971. Contact: Wing RA Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total hg bases = 422 Seq primer: AATTACCTCCTCCTAAGG High quality sequence stop: 555. Location/Qualifiers			
FEATURES	1..715			
SOURCE	/organism="Hordeum vulgare" /cultivar="CI16151 (Mla6)" /db_xref="taxon:4513" /clone="HV_CED0002K12f" /clone_1fb="Hordeum vulgare seedling green leaf EST library HVCDNA0005 (Blumeria challenged)" /issue_type="seedling green leaf" /lab_host="SOLR" /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI. C.I. 16151 (Mla6) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA: 7 day old green seedlings were challenged with isolate 5874 (AvrMla6) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give Bluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were played and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <a href="http://www.genome.clemson.edu/projects/barley">http://www.genome.clemson.edu/projects/barley</a> . To order this clone see <a href="http://www.genome.clemson.edu/orders">http://www.genome.clemson.edu/orders</a> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. ( <a href="http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html">http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html</a> )"			

Query Match		22.8%; Score 309.2; DB 9; Length 715;	
Best Local Similarity		79.7%; Pred. No.5,3e-69;	
Matches	365; Conservative	0; Mismatches	93; Indels
		0; Gaps	0;
QY	13	CCGAGTGCAGCGCCGCCACCGAGCAGCACCCCGCAGCGCGCGGATCCGACCTACCG	72
Db	103	CCGCGTGCCTCCCGCGGGGGAGACCCTGTCGAGAGCAATCGCGCGAGCTGCC	162
QY	73	AGGCGACGGTGCAGCAGGTGAGAGATGAAAGTGGAGGCCAGGTTGGGACATCTAC	132
Db	163	CGGCTCACCGTACACAGGTGAGAGATGAAGGTGGAGGCGGGGTAGCCGACATCTAC	222
QY	133	CGCTCCCTCTTCGGGGCGCGCCAAACAGAAATTCATCATCATAGACCTGTGGCGTAT	192
Db	223	CGCGTCTCTTTCGAGCGCGCGCCCAACCGCAAGTCCGCTGCTGGAGCTCTGGGCGCAT	282
QY	193	CAGCATATGCAGTATCTGACCGCTGGGCTGAGGCATATGGGACACAGCTTTCATGTTCTA	252
Db	283	CAGCATATGCAGTATCTGACGAAAGGCGCTGAGGCACTTGGCACCTGATCTGCTC	342
QY	253	GATGCAATGCGCCCTGGCTATGCTACGTGAGTATGTTCCATCTTGCTGATGAA	312
Db	313	GATGCAACCGACCTTGTTGTTGCTATTTGATGGCTTGACATGCTGGATGAA	402
QY	313	GCACCTGATGATGATCTTGCAGATATGATATCATATAGACTCTTACGTGCATATGATGAA	372
Db	403	ACGCTTGACATGACCTGAGAGACATATTTGAGACCTTCTGTCGATGCGAGACAAA	462
QY	373	GATGCTGATATATGTTGGTGCACCTGGACAGTTGGCTCACTAGCTAGCATTTATGCTGCT	432
Db	463	CATGCTGATATATGTTGGTGCACCTGGGACGATTTACTCATCTGCTACATATCATATGATGCTGCT	522
QY	433	GTAATATACATTTGTACATATGGGAGCGGAAGAGAT	470
Db	523	GTAATATACATTTGTACATATGGGAGTGAAGAAAGCACT	560
RESULT 4			
LOCUS	BF634888	694 bp	mRNA linear EST 19-DEC-2000
DEFINITION	NF075H10DT1F1091 Drought Medicago truncatula cDNA clone NF075H10DT		
ACCESSION	BF634888		
VERSION	BF634888		
KEYWORDS	BF634888.1 GI:11899046		
SOURCE	ESF.		
ORGANISM	barrel medic.		
	Medicago truncatula		
	Eunaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;		
	Medicago.		
REFERENCE	1 (bases 1 to 694)		
AUTHORS	Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,		
	Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.		
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation		
	Medicago truncatula drought library		
JOURNAL	unpublished (2000)		
COMMENT	Contact: May GD		
	Plant Biology Division		
	The Samuel Roberts Noble Foundation		
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA		
	Tel: 580 221 7391		
	Fax: 580 221 7380		
	Email: gdamay@noble.org		
	Insert Length: 694 Std Error: 0.00		
	Plate: 075 ROW: H COLUMN: 10		
FEATURES	Seq primer: TCACACAGGAAGACGCTGTGAC.		
	Location/Qualifiers		
	1..694		
	/organism="Medicago truncatula"		
	/db_xref="taxon:3880"		
	/clone="NF075H10DT"		







/note="Vector: plasmid pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI; mRNA was made from developing caryopses (3'-15'DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb. Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'- and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"

BASE COUNT 174 a 148 c 142 g 174 t 1 others  
ORIGIN

Query Match 18.7% Score 254; DB 9; Length 639;  
Best Local Similarity 78.6% Pred. No. 9e-55;  
Matches 316; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 959 GAGAGATGCTGCGACGACGATTCATATGGTCCACCGGAAAAAGTTCCTCTGCTG 1018  
DB 588 GATTGGTGTCTGGGACGACGCTATCTGGGTCCTGAGAAAAATCTCTATCG 529  
QY 1019 TGCATATGCGAAGTTGATTTGATTTT-ATACACAGACAGCAAAATGGCCACTC 1077  
DB 528 TGGATTATGTAAGTTGATTTGATTTTATGAGACAGACCAATAGGCCCTG 469  
QY 1078 TTCCATACATATGCGCTGACACAAATACATCTTGTCTCAGTACAGAGAGCC 1137  
DB 468 TTCACAAACATCTGCTGACCAATACATCTGCTTGGCGACAGTGTGAGAGAGA 409  
QY 1138 TTGAGGATAGCTGGAAGAAACAGATACATATCATCTACTGCTGCTAGTGGC 1197  
DB 408 TTGAGGATAGCTGGAAGAAACAGATACATCTGCTTGGCGACAGTGTGAGAGAGA 349  
QY 1198 CTCGACATGACGAGTACGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257  
DB 348 CTCGACATGACGAGTACGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 289  
QY 1258 GTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317  
DB 288 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 229  
QY 1318 GATAGTACCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359  
DB 228 GAGAAATACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187

RESULT 8  
BG095687 639 bp mRNA linear EST 29-JAN-2001  
LOCUS EST450122 potato leaves and petioles Solanum tuberosum cDNA clone  
DEFINITION cSTB38B18 5' sequence, mRNA sequence.  
ACCESSION BG095687  
VERSION BG095687.1 GI:12585636  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 639)  
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Lang, F., Cho, J.,  
Utterback, T., Hansen, C.L., Doan, B., Bougril, O., Buell, C.R., Rinning,  
C.M., Fry, W.E., Tankley, S.D. and Baker, B.  
Generation of ESTs from potato leaves and petioles  
Unpublished (2000)  
CONTACT: Cathy Rinning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com.  
location/Qualifiers  
1.639  
/organism="Solanum tuberosum"

/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="cSTB38B18"  
/clone\_lib="potato leaves and petioles"  
/tissue\_type="leaflets and petioles"  
/dev\_stage="8 weeks old plants"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; Tissue was supplied by Dr. Fry (Cornell University).  
Leaflets and petioles were isolated from 8 week old  
greenhouse grown plants. The plants were watered and  
fertilized freely. The tissue was immediately frozen in  
liquid nitrogen."

BASE COUNT 174 a 119 c 161 g 185 t  
ORIGIN

Query Match 18.2% Score 248; DB 10; Length 639;  
Best Local Similarity 66.9% Pred. No. 3.2e-53;  
Matches 353; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 72 GAGCTCAGCGTGCAGCGAGTGCAGATGAAGTGGAGCGCAGGCTGGCGACATCTA 131  
DB 83 GAAAGTACGAAAGCGCTGGAAATCAATGATGGTGGAGCGTGAATCCGAGAGATATA 142  
QY 132 CCGCTCCCTCTTCGCGGCCGCCCAACGAAATCCATCATGCTAGAGCTGGCTGA 191  
DB 143 CGATTATTTTACAGATTTTCCCAATTCCTGTCGACCTCATAGAGCTGGAACCTGA 202  
QY 192 TCACCATATGAGATATGACGCGCTGAGCATATGGAGACACCTTCATGTTCT 251  
DB 203 CAACACATTTGATTTATTTAGCCAAAGTCTCAGATTAAGTGTGCTGCTTCCGTTT 262  
QY 252 AGATGCCATGCGCTTGGCTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 311  
DB 263 GAGTGCAGAGTGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 322  
QY 312 AGCATGATGATGATGCTTGAATGATATCATGATGCTTCTAGCTGATGATGA 371  
DB 323 ATCTATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 382  
QY 372 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431  
DB 383 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 442  
QY 432 TGTAAATACATTTGTCGCAATAGGAGCGAAAGCATTTGTCATCAATCAATAGGCGAA 491  
DB 443 AGTCAATTCACCTATTAATCTTTGGCAAAAGCTGAAAGCTGTCATCAATTAATAGAGAAA 502  
QY 492 CCTGACATTTTATGCTGCAATAGGAGCGAAAGCATTTGTCATCAATCAATAGGCGAA 551  
DB 503 ATTCTACACATTTTGTGCGAAAGGAGCGAAAGCTGTCATCAATTAATAGGCGAA 562  
QY 552 TGGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599  
DB 563 TGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610

RESULT 9  
BE129712 521 bp mRNA linear EST 21-JUN-2000  
LOCUS BE129712/c 946003D09.XI 946 - tassels primordium prepared by Schmidt lab Zea  
DEFINITION BE129712 mRNA sequence.  
ACCESSION BE129712  
VERSION BE129712.1 GI:8577075  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 521)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University  
COMMENT Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu  
Plate: 946003 row: D column: 09.  
Location/Qualifiers

FEATURES  
source  
1. .521  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="946 - tassels primordium prepared by schmidt  
lb"  
/tissue\_type="tassels"  
/dev\_stage="just after the transition from vegetative to  
inflorescence development"  
/lab\_host="XLOLR"  
/note="Organ: tassels; Vector: HybridZAP; Site\_1: EcorI;  
Site\_2: XhoI; George Chuck dissected immature tassels  
between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
library in HybridZAP. Sample insert size range was 350 bp  
to 3 Kb with a 1 Kb average."  
118 c 97 g 155 t

BASE COUNT 151 a 118 c 97 g 155 t  
ORIGIN

Query Match 17.8%; Score 242; DB 9; Length 521;  
Best Local Similarity 100.0%; Pred. No. 1e-51;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1118 CTCAGTACTAGAGGAGGAGGCTTGAGGATTAAGCTGGAAGACAGAGATCATCATTT 1177  
|||||  
Db 371 CTCAGTACTAGAGGAGGAGGCTTGAGGATTAAGCTGGAAGACAGAGATCATCATTT 312  
|||||  
QY 1178 CATGCTACTGCTCAGTGCGCTCGCAGTTAGCCAGTACAGTGCAGTATGATCTGTT 1237  
|||||  
Db 311 CATGCTACTGCTCAGTGCGCTCGCAGTTAGCCAGTACAGTGCAGTATGATCTGTT 252  
|||||  
QY 1238 CGTGCCATTACCTCAGATGTGCTTGAGCCGTCTTAATTTCTGGAGCCATTCATC 1297  
|||||  
Db 251 CGTGCCATTACCTCAGATGTGCTTGAGCCGTCTTAATTTCTGGAGCCATTCATC 192  
|||||  
QY 1298 CACTCTACAATGTTGCTCTAGATAGTACCATACAGCCTATGATGTTCTCAGAAGAGT 1357  
|||||  
Db 191 CACTCTACAATGTTGCTCTAGATAGTACCATACAGCCTATGATGTTCTCAGAAGAGT 132  
|||||  
QY 1358 GA 1359  
||  
Db 131 GA 130

RESULT 10  
AM120078 533 bp mRNA linear EST 22-Oct-1999  
LOCUS AM120078  
DEFINITION 614083B05.y1 614 - root cDNA library from Walbot lab Zea mays cDNA,  
mRNA sequence.  
ACCESSION AM120078  
VERSION AM120078.1 GI:6095411  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 533)  
TITLE Walbot, V.  
AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford  
UNIVERSITY University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V

Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu  
Plate: 614083 row: B column: 05.  
Location/Qualifiers

FEATURES  
source  
1. .533  
/organism="Zea mays"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
/clone\_lib="614 - root cDNA library from Walbot lab"  
/tissue\_type="root"  
/dev\_stage="3-4 days old"  
/lab\_host="XLOLR"  
/note="Organ: root; Vector: p Bluescript II SK+; Site\_1:  
EcorI; Site\_2: XhoI; 3-4 days old root tissue from Walbot  
lab (LM)"  
157 a 109 c 103 g 162 t 2 others

BASE COUNT 157 a 109 c 103 g 162 t 2 others  
ORIGIN

Query Match 17.1%; Score 232; DB 9; Length 533;  
Best Local Similarity 100.0%; Pred. No. 4e-49;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1118 CTCAGTACTAGAGGAGGAGGCTTGAGGATTAAGCTGGAAGACAGAGATCATCATTT 1177  
|||||  
Db 302 CTCAGTACTAGAGGAGGAGGCTTGAGGATTAAGCTGGAAGACAGAGATCATCATTT 361  
|||||  
QY 1178 CATGCTACTGCTCAGTGCGCTCGCAGTTAGCCAGTACAGTGCAGTATGATCTGTT 1237  
|||||  
Db 362 CATGCTACTGCTCAGTGCGCTCGCAGTTAGCCAGTACAGTGCAGTATGATCTGTT 421  
|||||  
QY 1238 CGTGCCATTACCTCAGATGTGCTTGAGCCGTCTTAATTTCTGGAGCCATTCATC 1297  
|||||  
Db 422 CGTGCCATTACCTCAGATGTGCTTGAGCCGTCTTAATTTCTGGAGCCATTCATC 481  
|||||  
QY 1298 CACTCTACAATGTTGCTCTAGATAGTACCATACAGCCTATGATGTTCTTC 1349  
|||||  
Db 482 CACTCTACAATGTTGCTCTAGATAGTACCATACAGCCTATGATGTTCTTC 533  
|||||

RESULT 11  
BM177970 506 bp mRNA linear EST 06-DEC-2001  
LOCUS BM177970  
DEFINITION sa167e09.y1 Gm-c1072 Glycine max cDNA clone SOYBEAN CLOVE ID:  
Gm-c1072-4818.5; similar to SW-PTTB\_PEA 004903 PROTEIN  
FARNESYLTRANSFERASE BETA SUBUNIT ;, mRNA sequence.  
ACCESSION BM177970  
VERSION BM177970.1 GI:17401188  
KEYWORDS EST.  
SOURCE soybean.  
ORGANISM Glycine max

REFERENCE  
1 (bases 1 to 506)  
TITLE Shoenmaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna  
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers  
Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk  
R., Riteyer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann  
R., Waterston, R. and Wilson, R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoenmaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: east@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact: cures@resgen.com web site:  
www.resgen.com  
Seq primer: -40RP from GIBCO  
High quality sequence stop: 421.

## FEATURES

## SOURCE

Location/Qualifiers  
1. 506  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl072-4818"  
/clone\_lib="Gm-cl072"  
/tissue\_type="seedlings induced for symptoms of SDS  
(Sudden Death Syndrome) disease"  
/dev\_stage="2-3 weeks old"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI. The cDNA library was constructed from mRNA isolated  
from 2-3 week old seedlings that were induced for symptoms  
of SDS (Sudden Death Syndrome) disease by the  
translocation of culture filtrate of Fusarium solani f.  
sp. glycines (Plant Cell Report 18:375-380). Cultivar PI  
567374 is partially resistant to the disease SDS. Plant  
tissue (expanded leaves, folded leaves, and new shoots)  
were collected at 1, 6, 24, and 48 hrs. after inoculation  
and their mRNA pooled equally for cDNA construction. The  
library was prepared using the Stratagene pBluescript II  
SK(+) library construction kit. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) sequence with an XhoI restriction site. EcoRI  
adaptors were ligated to the blunt-ended cDNA fragments  
followed by XhoI digestion. The cDNA insert is protected  
from XhoI digestion via methylation during first strand  
synthesis. The cDNA fragments were directionally cloned  
into the EcoRI-XhoI restriction site of the pBluescript  
vector. The ligated cDNA fragments were transformed into  
E. coli Electromax DH10B host cells. Plants were inoculated  
by Shuxian Li (Glen Hartman lab, University of Illinois).  
Library was constructed by Steve Clough (Lila Vokhlin lab,  
University of Illinois)."

BASE COUNT 121 a 121 c 116 g 148 t  
ORIGIN

Query Match 15.6%; Score 225.8; DB 10; Length 506;  
Best Local Similarity 65.7%; Pred. No. 1.5e-47;  
Matches 329; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

```

OY 127 ATCTACCGCTGCGCTTCGGGGCGCGCGCAACGAAATCCATGCTAGAGCTGCG 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 ATTTACCACTCTTGGCCACCATTCCTCGCAACGCCCAACCCCTCATTTGGAGCTTCAA 61
OY 187 CGTGATCGCATTCAGATATCTGACGCGCTGGGAGCATATGACGACGCTTTCAT 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 CGCGATATTCACATGACATATGTCGCAAGGCGCTGCCATCTCAGTCCGCAATTTCC 121
OY 247 GTTCTAGATGCCAATGCCCTTGGCTATGCTAGTGGATGTTTCATCCATTCCTTGGCTG 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 GTTTGGAGCGCTAATCGACCCCTGCTGCTAGTGGATCTTCCACTCATTCGTTTGGCG 181
OY 307 GATGAGCACTTGATGATGATCTTGAGAAATGATATCATAGACTCTTACGTCGATGTCAG 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 GGAGAAATCCGATGATGATGAACTGAAAGATGAACTGATTTCTTAACCGTTGGCCAG 241
OY 367 GATAAAGATGGATATAGTGTGAGACCTGACAGATGCTCTCACTGATGACGATAT 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 GATCGAATGGTGGATATGGCGGGGAGACGACGATGCTCATATTCGCAACAATTAAT 301
OY 427 GCTGCTGTAATACACTTGTGACAATAGGAGCGAAGAGCATTTGTCATCAATCAATAGG 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 GCTGCTGTAATACACTTGTGACAATAGGAGCGAAGATCCCTGATCAATTAATAGGA 361
OY 487 GGCAAAGCTGTCAATTTTATGCTGCAATGAAAGATGATAGGTGCTTTGAGATGATGAT 546
```

```

Db 362 GATAAAGCTGTAGGCTTCTCGCGCGATGAAAGCAACCAATGCTGATAGATGAT 421
OY 547 GATGCTGCGCAAAATTTGATGCTCGGCTGCTCAACCCGCTATATGCGTGGCCAGCGTTG 606
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 GATGAGGTGAAATTTGATGCTTCGACCTTGTACACTGCACTTTCTGTGCAAGTGTTTG 481
OY 607 AATATTTCTGATTTTAACTG 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 AACATTTTGGATGATGACCTG 502
```

## RESULT 12

BF097538  
LOCUS

DEFINITION EST415611 tomato nutrient deficient roots Lycopersicon esculentum  
cDNA clone CLEM22H17 5' sequence similar to beta subunit of protein  
farnesyl transferase (Arabidopsis thaliana), mRNA sequence.

## ACCESSION

BF097538  
VERSION

## KEYWORDS

BF097538.1 GI:10903248  
EST.

## SOURCE

tomato.  
Lycopersicon esculentum

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum;  
Lycopersicon.

## REFERENCE

1 (bases 1 to 488)  
van der Hoeven,R.S., Garvin,D.F., Matern,A.L., Holt,I.E., Liang,F.,  
Upton,J., Hansen,T.S., Romling,C.M., Craven,K.B., Bowman,C.L.,  
Niernan,W., Fraser,C.M., Venter,J.C., Martin,G.B., Giovannoni,J.J.  
and Tanksley,S.D.  
Generation of ESTs from tomato nutrient-deficient roots  
Contact: CUGI

## AUTHORS

Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.

## TITLE

Generation of ESTs from tomato nutrient-deficient roots

## JOURNAL

Published (1999)

## COMMENT

Contact: CUGI

## FEATURES

source

## ORIGIN

1. 488  
/organism="Lycopersicon esculentum"  
/cultivar="TA492"  
/db\_xref="taxon:4081"  
/clone="CLEM22H17"  
/clone\_lib="tomato nutrient deficient roots"  
/tissue\_type="roots"  
/dev\_stage="5-6 weeks old"  
/lab\_host="SOLR"  
/note="Vector: pBluescriptSkmCudaapt; Site 1: 5' EcoRI;  
Site 2: 3' XhoI; Roots were harvested from plants grown  
under the following deficiencies/stresses: 10 mM Al, Zn,  
P, K, Fe, N. mRNA was isolated from individual treatments.  
Proportional aliquots of mRNA of each treatment were mixed  
and used for library construction."

## BASE COUNT

132 a 102 c 122 g 132 t

Query Match 15.9%; Score 215.6; DB 10; Length 488;  
Best Local Similarity 65.7%; Pred. No. 6.5e-45;  
Matches 314; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

```

OY 72 GAGCTCAGCGTGAAGGAGTGAGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 GAAAGTGAGGAAGAGCGGAGGAATGATGAGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 70
OY 132 CCGGCTCCTCTTGGGGGCGCGCCCAACAGCAATTCATATGCTAAGAGCTGTGGCGTGA 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 CGATTATTTCTACAGCAATTTCCCAACTCTCCCTCCGACCTCATAGAGATGCAAGCTGA 130
OY 192 TCACCATATGAGATGATGAGCGCTGGGCTGAGGATATGAGGAGGAGGAGGAGGAGGAG 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 CAAGCACTTGGTATCTAAGCCAAAGGCTTCAGAAAGCTGTGGTCCGTTTCCGTTT 190
```

```

OY 252 AGATGCCAATCGCCCTGGCTATGCTAGCTGATGGTTCATCCATTGCTTGGCTGATGA 311
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 GATGCGACAGTCACATGCTTGTCTAGTGACACTTCATTCATGCTTGTGGAGCA 250
OY 312 AGACTTGATGATGATCTTGAGATATATCATAGACTTCTTACGCTGATGATGA 371
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 ATCTATTTGGGGGAACTGAAATGATGATGATGATGATGATGATGATGATGATGAT 310
OY 372 AGATGCTGATATAGTGTGACCTGACACAGTTCCTCACCCTAGCTAGCTATGCTGC 431
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 AGATGCTGCTGATGAGAGTGACCTGCTGATGATGATGATGATGATGATGATGATGAT 370
OY 432 TGTAAATACACTTGTGACATAGGAGCGAAGAGCATTTGTATCATCATCATAGGCGCAA 491
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 AGCAATTCATCTAATTAATCTTGGGCAACCTGAGCTCTGTCATCATTAATAGAGAAA 430
OY 492 CCGTGTCAATTTATGCTGACATGAAAGTGTATCAGGCTCTTACAGATGATGAT 549
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 GTTGTACATATTTTCTGCGAATGAAAGCAGAGTGTGATGATGATGATGATGAT 488

RESULT 13
A1488509 457 bp mRNA linear EST 18-MAY-2001
LOCUS EST246848 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
DEFINITION CLE23124, mRNA sequence.
ACCESSION A1488509
VERSION A1488509.1 GI:4383880
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eunsterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 457)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Rongling,C.M., Craven,M.B., Fujii,C.Y., Bowman
,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES
source
1..457
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone_lib="tomato ovary, TAMU"
/clone="CLE23124"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="X11-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLED - Tomato Carpel EST library. OligoRT-pimed and
directionally cloned cDNA in vector lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."
BASE COUNT 121 a 99 c 111 g 126 t
ORIGIN
Query Match 15.6%; Score 211.8; DB 9; Length 457;
Best Local Similarity 66.6%; Pred. No. 6e-44;
Matches 303; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
OY 100 ATGAGGTGAGGCGAGGCTTGCGACATCTACCGCTCTTGGGCGCGCCCAAC 159
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3 ACAGAGGTGAGGCGTGCAGTCCGAGATATTCGATTATTTCTACAGCATTTCCCAAC 62

```

```

OY 160 ACGAAATCCATCATGCTGAGCTGTGGCTGATCAGCATTCGATCTGACGCTGGG 219
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 63 TCTCCGCGCACTCATATAGATGATGAAAGTGAACGATGAAACACTTGGTTATCTAACGCAAGT 122
OY 220 CTGAGGCATATGGGACCGACCTTTATGTTCTTCTAGATGCCAATGCGCTTGGTATGCTAC 279
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 123 CTGAGAAACCTTGGTCCGCTTCTTCCCTTGGTGGATGCCAGTGCAGCATGCTTGGCTAC 182
OY 280 TGGATGGTTCATCTGCTGCTTGGTGGATGAAGCACTTGATGATGATGATGATGATGAT 339
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 183 TGGACACTTATTCATTCGCTTGTGGGAAATCTATTGTGGCAAACTGGAAATGAT 242
OY 340 ATCATGACTTCTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 399
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 243 GCAATGACTTCTTGAACCCCTTGCCAGAGATGAAGATGATGATGATGATGATGATGATGAT 302
OY 400 CAGTGGCTCCTACCTAGCTACGACTTATGCTGCTGTAATATCACTTGTGACATAGGAGC 459
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 303 CAGATGCTTCATCTTGCATCACTTATGCTGACAGTCAATTCATCACTTATCACTTGTGCGCAA 362
OY 460 GAAAGACATTTGTCATCAATCAATGAGGCGCACTGACATTTTATGCTGCGAGATGAAA 519
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 363 CCGAAGCTCTGTCATCAATTAATAGAGAAAGTTGTACACATTTTGTGCGAATGAAA 422
OY 520 GATGTATCAGGTGCTTTCAGAAATGATGATGATGATGATGATGATGATGATGATGAT 554
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 423 GACGCAAGTGTGATGATCAAGATGACAGATGATGATGATGATGATGATGATGATGAT 457

RESULT 14
BC013574 2707 bp mRNA linear HTC 07-SEP-2001
LOCUS BC013574
DEFINITION Homo sapiens, farnesyltransferase, CAAX box, beta, clone
IMAGE:3898137, mRNA.
ACCESSION BC013574
VERSION BC013574.1 GI:15488887
KEYWORDS HTC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2707)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) md@paxil.stanford.edu
Dickson, M., Schmitz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAK Plate: 14 Row: K Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 292032
This clone has the following problem: incomplete processing.
FEATURES
source
1..2707
/organism="Homo sapiens"
/db_xref="locusID:2342"
/db_xref="taxon:9606"

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/clone="IMAGE:3898137"
/issue_type="Pancreas, epithelioid carcinoma"
/clone_lib="NH_MGC_70"
/lab_host="DH10B"
/notes="Vector: PCMV-SPORT6"

BASE COUNT      628 a      743 c      692 g      644 t
ORIGIN

Query Match      14.9% Score 202; DB 11; Length 2707;
Best Local Similarity 56.4% Pred. No. 5.2e-41;
Matches 398; Conservative 0; Mismatches 305; Indels 3; Gaps 1;

QY 172 ATGCTAGACGCTGGCGTGCATACCATATCGATATCTGACCGCTGGCGGCATATG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 AGCGTTGTTTTCAGAGAGGAGCAACCTTCTCATTTCTGAAAGAGCGCTCGACACTG 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 232 GGACGAGCGCTTTCATGTTCTAGATGCCAATGGCCCTAGTCTACTGATGATGTTT 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 ACAGATGCTTATGAGTGTCTGATGCCAGCGCCCATGGCTCTGCTATTTGATCTCGAC 365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 292 CCACCTTCCTTTCATGATGAACGACATTTGATGATGATCTTGAATATCATAGACTTC 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 AGCTTGGAGCTGATAGATGAACCCATCCCGCAGATAGTGGCTACAGATGCTGTCACTTC 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 352 TTACCTGATGTCAGATTAAGATGTGATATAGTGGTGGACCTGGACAGCTTCCCTCAC 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 CTGAGGCTGTCTCAGACCCCGCAAGGTGGCTTTGGAGAGAGACCCGCTCATATCCACAC 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 412 CTACCTAGCACTTATGCTGCTTAATACACTTGTGACATAGAGGAGGAGCAAGACATG 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 CTTGACCCCATATATGACGACGATACATTTGCTATTCATTTGGACCGACGAGCGCTAT 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 TCATCATCAATAGAGGCAACCTGTACAAATTTTATGCTGCAGATGAAGATGTATCAGCT 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 546 GACATCATTTAACAGAGAAAGCTTCTTCAGATTTTGTACTCCCTGAAGCAACCTGACGGC 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 GCTTTCAGATGATGATGCGGGAATTTGATGTCGCTTCTTACACCGCTATATCG 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 606 TCCCTTTCATGATGTCGAGGAGGTGATGTGAGAACCGCATCTGTGCGCTCC 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 592 GTTCCAGACCTTTCGATATTTCTTGAATTTTAACTGGCAAAAGSTGAGGCACTACATA 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 666 GTACCTTCGCTGACCAACATCATCTCCAGACCTCTTTAGGGCACTGCTGATGATGATA 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 652 GCAAGTGTCAAACTATGAAGGTGATGTCGCGGAGCCCTTATGCTGAAGCAATGCT 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 726 GCAAGGTGTCAAGACTGGAGAGGTGGCATTTGGCGGGTACAGAGGATGAAGCCCATAGCT 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 712 GGGATATCATTTCTGATGCTGCTGCTTTGATCTCTGCTTAATGAGCAAGAAAGTTGAC 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 786 GGGATATCATTTCTGATGCTGCTGCTGCGCGCTGTATCTCAAGAGGAAAGCTTCTTGAAC 845
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 772 TTGCTATGTTTGAATGGCTGGTGGCTTTTCTGTCATCA--AGAGTGAAGTGGATTTCAA 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 846 TTGAAGAGCTTATTAACATGGGTGACAAAGCGGACAGATGCGATTTGAAGAGGATTTGAG 905
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 829 GGAGCAACTAATAATTGTTGATGTTGCTACTCTTTTGGCAGG 874
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 906 GGCGGCTGCAACAGCTGTGTGATGCTGTACTCTTCTGGCAGG 951
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
AM508684      553 bp      mRNA      linear      EST 03-DEC-2001
LOCUS      s135b06.y1 Gm-r1030 glycine max cdna clone GENOME SYSTEMS CLONE ID:
DEFINITION      Gm-r1030-876 5' similar to SW:PTA_PEA 004903 PROTEIN
FARNESYLTRANSFERASE BETA SUBUNIT ;, mRNA sequence.
ACCESSION      AM508684
VERSION      AM508684.1 GI:7146762
KEYWORDS      EST.
SOURCE      soybean.
ORGANISM      Glycine max
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

```
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 553)
REFERENCE      Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
AUTHORS      A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
             Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
             Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk
             R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
             R., Waterston, R. and Wilson, R.
TITLE      Public Soybean EST Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
             Public Soybean EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: estewatson.wustl.edu
             This clone is available through: ResGen, Invitrogen Corp. 2130
             South Memorial Parkway Huntville, AL 35801 For further information
             call: (800)-533-4363 or contact via email: cou@resgen.com
             Insert Length: 1739 Std Error: 0.00
             High quality sequence stop: 430.
             Location/Qualifiers
               1..553
               /organism="Glycine max"
               /db_xref="taxon:3847"
               /clone="GENOME SYSTEMS CLONE ID: Gm-r1030-876"
               /clone_lib="Gm-r1030"
               /lab_host="DH10B"
               /note="Vector: PSORT1; Site_1: SalI; Site_2: NotI; This
             cdna library was constructed from mRNA isolated from
             immature cotyledons of greenhouse grown plants
             (individual seed fresh weight of 100-300mg). The library
             was prepared using the Life Technologies PSuperScript cdna
             library construction kit. Complementary DNA was
             synthesized from mRNA using a poly(dT) sequence with a
             NotI restriction site. SalI linkers adapters were ligated
             to the blunt-ended cdna fragments followed by NotI
             digestion. The cdna fragments were directionally cloned
             into the NotI-SalI restriction site of the pSPORT1
             vector. The ligated cdna fragments were transformed into
             E. coli Electromax DH10B host cells. This library was
             constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note
             that Gm-r1030 is a re-track of Gm-cl007."

BASE COUNT      131 a      139 c      141 g      142 t
ORIGIN

Query Match      13.8% Score 188; DB 9; Length 553;
Best Local Similarity 63.2% Pred. No. 9.4e-38;
Matches 306; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

QY 70 CCGAGGCTCAGCGTGAGCAGGTGAGCAGATGAAGTGGAGCGGCTTGGCAGATC 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 CCGGTTCGACGGGTGATCAACGTGACATGATGATGATGATGATGATGATGATGATGAT 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130 TACCGCTCCCTCTTTCGCGCGCGCGCCACGCAAAATCATCATGTAGAGCTGTGGCGT 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 TACCAACTTTCGCGCACCATTTCTCCGCAAGCCCTTCGCAATGTTCCGATTTTCCGTT 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 190 GATCAGCATATTCAGATATCTGACGCGCTGAGGCTATGAGGACCAAGCTTTATGTT 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 GATTAATCATCATGAGATGATGCTCCAAAGGCTTCGCAATGTTCCGATTTTCCGTT 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 250 CTAGATGCCCAATGGCCCTTGGCTATGCTATGATGATGATGATGATGATGATGATGAT 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 TTGGACGCTATATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 310 GAAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 310 GAATCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```

QY 370 AAAGATGCTGATATATGCTGGACCTGGACAGTTCCTACCTAGCTAGACTTATGCT 429
    |||||
Db 370 CCGAATGGTGATATGCCGGGGGACCGCCAGATGCTCATATTCACACACTTATGCT 429
    |||||
QY 430 GCTGTAATACACTTGTGACAAATAGGGAGCGAAAGAGCATTTGTCATCAATCAATAGC--- 486
    |||||
Db 430 GCTGTAATTCACCTTATTTACTTTGGTGTGAGAAATCCCTGGCATCAATTAATAGGTGA 489
    |||||
QY 487 GGCACCTGTACAAATTTTATGCTGCAGATGAAAGATGTATCAGGTGCTTTCAGAAATGCAT 546
    |||||
Db 490 GATTAACCTSTATGGTTTCTCGCGCGGATGAACCAACAATGTGTGATTCAGGATGCAT 549
    |||||
QY 547 GATG 550
    |||||
Db 550 GATG 553
    |||||

```

Search completed: November 1, 2002, 14:50:42  
 Job time : 1804 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 16:23:35 ; Search time 50 Seconds

(without alignments)  
1004.107 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411  
Sequence: 1 MDPSQSTPPYGDPPAAAD.....PLYNVVLDKRYTAYFFSEE 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

1: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1989.DAT:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2411	100.0	452	21	AAV70502
2	1368	56.7	429	21	AAV70504
3	1306	54.2	313	21	AAV70503
4	1205.5	50.0	443	21	AAV70506
5	1205.5	50.0	475	21	AAV70505
6	1192	49.4	444	21	AAV70507
7	1192	49.4	476	21	AAV70508
8	1163.5	48.3	405	21	AAV70509
9	1159.5	48.1	404	20	AAV70510
10	1150	47.7	406	20	AAV70511
11	944.5	39.2	437	15	AAV70512

12	942.5	39.1	437	15	AAV70513
13	942.5	39.1	437	16	AAV70514
14	942.5	39.1	437	17	AAV70515
15	940.5	39.0	437	15	AAV70516
16	935.5	38.8	440	15	AAV70517
17	898.5	37.3	387	16	AAV70518
18	898.5	37.3	387	17	AAV70519
19	896.5	37.2	387	15	AAV70520
20	832.5	34.5	419	22	AAV70521
21	763.5	31.7	298	21	AAV70522
22	756.5	31.4	291	21	AAV70523
23	719.5	29.8	282	21	AAV70524
24	443	18.4	141	21	AAV70525
25	359	14.9	355	22	AAV70526
26	345.5	14.3	321	21	AAV70527
27	343.5	14.2	313	21	AAV70528
28	340.5	14.1	317	21	AAV70529
29	336	13.9	300	21	AAV70530
30	334	13.9	287	21	AAV70531
31	330	13.7	299	21	AAV70532
32	320	13.3	377	16	AAV70533
33	320	13.3	377	17	AAV70534
34	313	13.0	376	17	AAV70535
35	313	13.0	377	16	AAV70536
36	304.5	12.6	313	22	AAV70537
37	304.5	12.6	347	22	AAV70538
38	291.5	12.1	318	22	AAV70539
39	286	11.9	395	22	AAV70540
40	285	11.8	291	22	AAV70541
41	189	7.8	384	20	AAV70542
42	101	4.2	590	22	AAV70543
43	97	4.0	253	20	AAV70544
44	96.5	4.0	2703	22	AAV70545
45	93.5	3.9	1379	22	AAV70546

# ALIGNMENTS

AAV70502	AAV70502 standard; Protein; 452 AA.
AC	AAV70502;
DT	04-JUL-2000 (first entry)
DE	Corn farnesyltransferase beta subunit.
XX	Corn; farnesyltransferase beta subunit; transgenic plant;
KW	drought tolerance; cell growth.
OS	Zea mays.
XX	WO200014207-A2.
PN	16-MAR-2000.
PD	07-SEP-1999; 99WO-US20419.
PF	08-SEP-1998; 98US-0099521.
PR	(DUPO) DU PONT DE NEMOURS & CO E. I.
PA	Cahoon RE, Miao G, Powell W;
PI	WPI; 2000-256964/22.
XX	N-PSDB; AA51791.
DR	New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT	useful for producing transgenic plants with an altered level of
PT	farnesyltransferase -
XX	

PS Claim 14: Page 39-40; 51pp; English.  
XX  
XX The present sequence is a farnesyltransferase beta subunit from  
CC clone p0127.cnbu.18r isolated from corn nucellus tissue cDNA library.  
CC The coding sequence of this protein is used in the construction  
CC of a chimeric gene to produce transgenic plants with altered level  
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase  
CC activity may have enhanced tolerance to drought stress. Nucleic acids  
CC encoding all or a part of farnesyltransferase proteins can be used in  
CC studies to understand cell growth in plants and provide genetic tools to  
CC control cell growth and improve tolerance to drought in mature plants.  
XX  
SQ Sequence 452 AA:  
Query Match 100.0%; Score 2411; DB 21; Length 452;  
Best Local Similarity 100.0%; Pred. No. 4e-238;  
Matches 452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDSPPOSTPTGDDPAAAPDLPRLTVTOYEQMKVVARVDITRSLFGAAPTNTKSTMLE 60  
DB 1 MDSPPOSTPTGDDPAAAPDLPRLTVTOYEQMKVVARVDITRSLFGAAPTNTKSTMLE 60  
QY 61 LMRDQHIETLPGLRHNGPAFHVLDANRPMICYMWHPLALDLDELDDLENDITDPLAR 120  
DB 61 LMRDQHIETLPGLRHNGPAFHVLDANRPMICYMWHPLALDLDELDDLENDITDPLAR 120  
QY 121 CQDKGGYSGGPGQLPHLATTYAANTLVITIGSERALSSINRGNLYNFMLOMKDVSGAPR 180  
DB 121 CQDKGGYSGGPGQLPHLATTYAANTLVITIGSERALSSINRGNLYNFMLOMKDVSGAPR 180  
QY 181 MHQGEIDVASTATISVASLVNLDLFLAKGVGDYIARQTYEGGJAGEPYAAHAGCYT 240  
DB 181 MHQGEIDVASTATISVASLVNLDLFLAKGVGDYIARQTYEGGJAGEPYAAHAGCYT 240  
QY 241 FCGLAALILNEAEKVDLPGLIGWAFRQGEFGQRTNKLVDGCSFPMOGAAIAFTOK 300  
DB 241 FCGLAALILNEAEKVDLPGLIGWAFRQGEFGQRTNKLVDGCSFPMOGAAIAFTOK 300  
QY 301 LITTVDKOLKSSYSCKRPSEDACTSSYGCCTAKKSSSAVDYAKFGDFITQOSNOIGPLF 360  
DB 301 LITTVDKOLKSSYSCKRPSEDACTSSYGCCTAKKSSSAVDYAKFGDFITQOSNOIGPLF 360  
QY 361 HNIALQOYILLCQVLEGGIRDKRGNRDYHSCYCLSGLAVSQYSAMTDTGSCPLQHV 420  
DB 361 HNIALQOYILLCQVLEGGIRDKRGNRDYHSCYCLSGLAVSQYSAMTDTGSCPLQHV 420  
QY 421 LGPYSNLEPIHPLYNVLDKYHTAYEFSEE 452  
DB 421 LGPYSNLEPIHPLYNVLDKYHTAYEFSEE 452  
RESULT 2  
AAV70504  
ID AAV70504 standard; Protein: 429 AA.  
XX  
XX AAV70504:  
XX  
XX 04-JUL-2000 (first entry)  
XX  
XX Soybean farnesyltransferase beta subunit from clone sfl1.pk0086.h10.  
XX  
XX KW Soybean; farnesyltransferase beta subunit; transgenic plant;  
XX drought tolerance; cell growth; clone sfl1.pk0086.h10.  
XX  
XX Glycine max.  
XX  
XX PN W0200014207-A2.  
XX  
XX PD 16-MAR-2000.  
XX  
XX PF 07-SEP-1999; 99WO-US20419.  
XX  
XX PR 08-SEP-1998; 98US-0099521.

XX  
PA (DUPO) DU PONT DE NEMOURS & CO E. I.  
XX  
XX Cahoon RE, Miao G, Powell W;  
XX  
XX WPI, 2000-256964/22.  
XX  
XX N-PSDB; AAZ51793.  
XX  
XX New isolated polynucleotide encoding farnesyltransferase polypeptide is  
XX useful for producing transgenic plants with an altered level of  
XX farnesyltransferase.  
XX  
PS Claim 14: Page 42-44; 51pp; English.  
XX  
XX  
XX The present sequence is a farnesyltransferase beta subunit  
XX from soybean clone sfl1.pk0086.h10.  
XX The coding sequence of this protein is used in the construction  
XX of a chimeric gene to produce transgenic plants with altered level  
XX of farnesyltransferase subunit. Plants with decreased farnesyltransferase  
XX activity may have enhanced tolerance to drought stress. Nucleic acids  
XX encoding all or a part of farnesyltransferase proteins can be used in  
XX studies to understand cell growth in plants and provide genetic tools to  
XX control cell growth and improve tolerance to drought in mature plants.  
XX  
SQ Sequence 429 AA:  
Query Match 56.7%; Score 1368; DB 21; Length 429;  
Best Local Similarity 60.5%; Pred. No. 3.3e-131;  
Matches 259; Conservative 63; Mismatches 94; Indels 12; Gaps 5;  
QY 36 VEARVGDITRSLGAP-NPKSTMLEMRDQHIETLPGLRHNGPAFHVLDANRPMICYW 94  
DB 2 VESQVFOIYO-LPATIPRNAQTLMLELRDQHIETLPGLRHNGPAFHVLDANRPMICYW 60  
QY 95 MVRPLALDLDELDDLENDITDPLARCQDKGGYSGGPGQLPHLATTYAANTLVITIGSE 154  
DB 95 MVRPLALDLDELDDLENDITDPLARCQDKGGYSGGPGQLPHLATTYAANTLVITIGSE 154  
QY 155 RALSSINRGNLYNFMLOMKDVSAFRMHQGEIDVASTATISVASLVNLDLFLAKGVG 214  
DB 155 RALSSINRGNLYNFMLOMKDVSAFRMHQGEIDVASTATISVASLVNLDLFLAKGVG 214  
QY 215 DYIARQTYEGGJAGEPYAAHAGCYTFCGLAALILNEAEKVDLPGLIGWAFRQGEFG 274  
DB 215 DYIARQTYEGGJAGEPYAAHAGCYTFCGLAALILNEAEKVDLPGLIGWAFRQGEFG 274  
QY 275 FQGRTNKLVNCGYSFPMOGAAIAFTOKLITTVDKOLKSSYSCKRPSEDACTSSY 329  
DB 275 FQGRTNKLVNCGYSFPMOGAAIAFTOKLITTVDKOLKSSYSCKRPSEDACTSSY 329  
QY 330 G-CTAK---KSSSAVDYAKFGDFITQOSNOIGPLHNIALQOYILLCQVLEGGIRDKP 384  
DB 330 G-CTAK---KSSSAVDYAKFGDFITQOSNOIGPLHNIALQOYILLCQVLEGGIRDKP 384  
QY 385 GKNRDYHSCYCLSGLAVSQYSAMTDTGSCPLQHVYGPYSNLEPIHPLYNVLDKYHT 444  
DB 385 GKNRDYHSCYCLSGLAVSQYSAMTDTGSCPLQHVYGPYSNLEPIHPLYNVLDKYHT 444  
QY 445 AVEEFSEE 452  
DB 445 AVEEFSEE 452  
QY 421 AHEFFTE 428  
DB 421 AHEFFTE 428  
RESULT 3  
AAV70503  
ID AAV70503 standard; Protein: 313 AA.  
XX  
XX AAV70503:  
XX  
XX 04-JUL-2000 (first entry)  
XX  
XX DE Rice farnesyltransferase beta subunit.  
XX

KW Rice; farnesyltransferase beta subunit; transgenic plant;  
KM drought tolerance; cell growth.  
XX  
OS Oryza sativa.  
XX  
PN MO200014207-A2.  
XX  
PD 16-MAR-2000.  
XX  
PF 07-SEP-1999; 99WO-US20419.  
XX  
PR 08-SEP-1998; 98US-0099521.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Cahoon RE, Miao G, Powell W;  
XX  
DR MPI: 2000-256964/22.  
XX  
DR N-PSDB; AA251792.  
XX  
PT New isolated polynucleotide encoding farnesyltransferase polypeptide is  
XX  
PT useful for producing transgenic plants with an altered level of  
XX  
PS farnesyltransferase -  
XX  
PS Claim 14; Page 41-42; 51pp; English.  
XX  
CC The present sequence is a farnesyltransferase beta subunit  
XX  
CC from clone r124.pk0007.d6 isolated from rice infected leaf cDNA library  
XX  
CC r124. The coding sequence of this protein is used in the construction  
XX  
CC of a chimeric gene to produce transgenic plants with altered level  
XX  
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase  
XX  
CC activity may have enhanced tolerance to drought stress. Nucleic acids  
XX  
CC encoding all or a part of farnesyltransferase proteins can be used in  
XX  
CC studies to understand cell growth in plants and provide genetic tools to  
XX  
CC control cell growth and improve tolerance to drought in mature plants.  
XX  
SQ Sequence 313 AA:  
  
Query Match 54.2%; Score 1306; DB 21; Length 313;  
Best Local Similarity 80.7%; Pred. No. 4,6e-125;  
Matches 247; Conservative 24; Mismatches 25; Indels 10; Gaps 4:  
  
OY 1 MDPSPTPTGGDPA-----AAD---PDLRLTYTOYEQMKVEARVGDITSLGAP 52  
DB 1 MDP-PSPPPPPPYPAABGGRPADSOAAELPLRLTYTOYEQMKVEAKVGEIYVLEGNAP 59  
OY 53 NTKSIMLELRDQHIETLPGLRHMGPATFVLDANRPMLCYMWVHPALDLDEALDDLEN 112  
DB 60 NANSMLLELRHQHVEYTLRGLKHGSPFHVLDANRPMLCYWIHALALLE-IPDDVED 118  
OY 113 DIIDPLARQODKDGYSGGPQLPHLATYYAAVNTLVTTIGSERALSSINGNLYNFMLOM 172  
DB 119 DIVDFLSRCODKGGYGGPGQLPHLATYYAAVNTLVTTIGSERALSSVNRDNLKFKMLRM 178  
OY 173 KDVSQAFRMHDSGEIDVRSATYASVSLVNIIDFLKAGVGYIARCQYEGGINGEPT 232  
DB 179 KDTSGAFRMHDSGEIDVRSATYASVSLVNIIDFLKAGVGYIARCQYEGGINGEPT 238  
OY 233 AEAHGGYTCGLAALILLEAEKVDLPSLIGWAFRGQVEGCGRGTNKLVDGCYSFWMG 292  
DB 239 AEAHGGYTCGLATWILLNEVDKLDLALIGWAFRGQVEGCGRGTNKLVDGCYSFWMG 298  
OY 293 AAIATFT 298  
DB 299 AALALT 304

DT 17-OCT-2000 (first entry)  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8715.  
XX  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
XX Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
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PR 23-MAR-1999; 99US-0125788.  
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PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
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Query Match          50.0%; Score 1205.5; DB 21; Length 443;
Best Local Similarity 51.7%; Pred. No. 1,6e-114;
Matches 232; Conservative 73; Mismatches 111; Indels 33; Gaps 3.

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Db       3 ELSSLTSSQREFPLEVENDYFGIYNWTFDASDVSTOKYMMIQRKDQIDYIMKGLRQGP  62

QY      82 HVLNANRPMLCYMWHPLDLALDEALDDDDLENIIDIFLARCODKDGSGSGPOLPLATT  141
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Db       63 SLDLNNRPLCYLWIIHSLALIGETVDDDELHSAINIDPLGRGQSGEGYGGPQQLPLATT  122

QY      142 YAAVNTLVLTIGSERALSSINRGNLNFMKIQMKDVSGAFPMHDGGLIDVRASTTAISVSL  201
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Db       123 YAAVNAVLTLLGDDKALLSSINREKMSQFLERMKDTSGCFPMHMGELIDVRACTTAISVASI  182

QY      202 VILIDFLKAGKGVDIARQOTYEGGJAGEPYAEAHGQYFFGCLAILILNKEAKVDLPSTL  261
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Db       183 LWMIDDELQGLGDYILSCQTYEGGJGGEPSGAHGYIYCGLAANITLLINEVDRLDLDSL  242

QY      262 IGMVAFRGQVEGCGPGGRTKKLVLDGCTSPFQAGAAIAFYQKLLITLVDKQLKSSYCKR----  317
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Db 243 MNMAVHQVEMGFQGRNKLVDGCTFMQAPVLLQRLYSTNDHDVHGSSHISEGNE 302  
QY 318 -----PGEADACTSSYGCTAKKSSAVDYANFGPDFIOOSNOICPLF 360  
Db 303 EHHAHDEDDLEDSDDDDDSDDEDSDVNGHRHHTST-----YINRRMQL--VF 350  
QY 361 HNTALQOYILLCSYLVLEGGLRDKRKNRDHYHSCYCSGLAVSOYSAMTGTGCPPLPOHV 420  
Db 351 DSLGLQRYLLCSKIPDGGFKPRKPRDFYHTCYCLSGLSVAOHAWMLKDEDTPPLTRDI 410  
QY 421 LGPYSNLEPIHPLYNVVLDKRYHAYEEF 449  
Db 411 MGSYNLEPVLQHLNVTMDOYNPAIEFF 439  
RESULT 5  
AAG10405  
ID AAG10405 standard; Protein: 475 AA.  
XX AAG10405;  
XX AC AAG10405;  
XX DT 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 8714.  
XX KM Protein identification: signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX Arabidopsis thaliana.  
XX OS EPI033405-A2.  
XX PN EPI033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
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PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match

50.0%; Score 1205.5; DB 21; Length 475;

Best Local Similarity 51.7%; Pred. No. 1,86-114;	
Matches 232; Conservative 73; Mismatches 111; Indels 33; Gaps 3;	
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DB	35 ELSSLVSQRDFLEVENVFGLYNYFDASDVSTOKYMEIQRDQLDLMKGLRQGF 94
QY	82 HVLDAARPMLCYMMVHPLALDEALDDLENDIIDFLARCDDKDGSGGPGQLPHLATT 141
DB	95 SSLDANRMLCYMILHSLALLGLEYDDELSAIDFLRCGSEGGGGGQLPHLATT 154
QY	142 YAAVNTLVITGSEKALSSINNGNLYNFMLOKMDVSGAFRMDGRIYRASATYASVL 201
DB	155 YAAVNTLVITGDKALSSINREKMSFLRMKDDTSRGFRMDGRIYRACATYASVSI 214
QY	202 VNIIDFKLAKGVGDYIACQTYEGGIAEPYAEANAGTTFEGGLAALLINAEKVDLPSL 261
DB	215 LNIIDDELTOGLGDYILSCQTYEGGIGEPSEANGYTYGGLAAMITINEVDRLNDSL 274
QY	262 IGWVAFROGVEGCFQGRNTKLVDCGYSFMOGALIAFTOKLITVDKOLKSSYSCKR 317
DB	275 MNMAVHRQGVEMGROGRNTKLVDCGYTMOAFCVLLDRLISTNDHVDHSGSHISEGNE 334
QY	318 -----PSGEDACSTSSYGCTAKKSSAVDYANAFGEFDIQOSMOIGPLF 360
DB	335 EHHAHDEDDLEDSDDDDDDEDNDEDSVNGHRIHHTST-----YINRMQL--VF 382
QY	361 HNIALQOYIILCSOYLKGLDKPGKNDHYHSCYCSGLAVSOYSAMTDGSCPLPOHV 420
DB	363 DSLGLRTVLCSSKIPDGGFRDKPRKPRDFYHTCTCLGLSVQAHAMUKDDEDTPLTRDI 442
QY	421 LGPYSNLEPIHPLYNVVLDRYHTAYEPF 449
DB	443 MGYSNLEPVPOLLHNIYMDQYNEAIEPF 471
RESULT 6	
AAG46813 standard; Protein: 444 AA.	
XX	AAG46813:
AC	18-OCT-2000 (first entry)
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 58934.
DE	Protein identification: signal transduction pathway; metabolic pathway;
KW	hybridisation assay: genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	Arabidopsis thaliana.
OS	Arabidopsis thaliana.
XX	EP1033405-A2.
PN	06-SEP-2000.
PD	25-FEB-2000; 2000EP-0301439.
XX	25-FEB-1999; 99US-0121825.
XX	05-MAR-1999; 99US-0123180.
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PR 29-OCT-1999; 99US-0162142.

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49.4%; Score 1192; DB 21; Length 444;

Best Local Similarity 51.3%; Pred. No. 3.9e-113;

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DB 3 ELSSLTYSQRPQFLVENDVFQIYVPDASVSTOKYMEIDRQOLDYLMKGLRQLPQPF 62  
QY 82 HVLDPANRPMLCMMVHPPLALDEALDDLENDIDFLARCODKGGYSGRPGQLPLATT 141  
DB 63 SSLDANRPMLCMWLHSLTALLGETVDELESNALIDFLGRCCSGGCGGQLPLATT 122  
QY 142 YAAVNTLVTTGSEPALSTIN-RGMLYNFMLOMKVSGAFRNHGDGEIDVRASYAISVAS 200  
DB 123 YAAVNAVLVTGGDKALSSINSREKMSCFLLRMKDTSCGFNMHDMGEMDVRACTAISVAS 182  
QY 201 LVNLDPLKMGVGDYIARCOYEGGAGERYAEAHGCTGCGLAALILLNEAKVQLPS 260  
DB 183 ILNIMDELDTGLDYLISCTYEGGIGGEPGSEAHGCTYCGLAAMLLINEVRLNIDS 242  
QY 261 LIGVAFROGVGECFOGRTNKLVDGCYSFWOGAAIAFTOKLITTVDRKSSYSCKR-- 317  
DB 243 LMNNAVHRQGVEMFOGRTNKLVDGCYTFWQARPCVLLDRYSTNDDHVSISHSECTN 302  
QY 318 -----PAGEDACTSSYGCCTAKKSSSAVDYAKFCGFDTIQGSGNQIGPL 359  
DB 303 EENHAHDEDDLEDDDDDDDEDDEDSDSVNGHRIHTST-----YINRMQL--V 350  
QY 360 FHNIALDOYILLCGSOVLEGGGRDRKRGKRNDRHYSCTGSLGVAOYSAMDTGSCPLPQH 419  
DB 351 FDSIGLQRYVLCSKIPDGGGRDRPKPRDPRYHHCYCLSGLSVAQHAWLKDETPPLTRD 410  
QY 420 VLGPYSNLEPRHPLVNVVLDKVTAYEFF 449  
DB 411 IMGYSNLEPRVQLHNINVMQYNEATIEFF 440

## RESULT 7

AAG46812 standard; Protein: 476 AA.

AAG46812:

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 58933.

Protein identification: signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

Arabidopsis thaliana.

PN EP1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
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PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.





OY 420 VLGPYSNLEPIHPLVNVLDKRTATATFF 449  
DB 443 IMCGSYNLEPVLHNIYMDQYNEAIEFF 472  
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ID AAG10407 standard; Protein; 405 AA.  
XX AAG10407;  
XX 17-OCT-2000 (first entry)  
DT  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 8716.  
XX  
XX Protein identification: signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
XX Arabidopsis thaliana.  
XX  
XX EPI033405-A2.  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 48.38; Score 1163.5; DB 21; Length 405;
Best Local Similarity 53.0%; Pred. No. 2,8e-110;
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QY 58 MLEIMROHIEYLTPLGRIHMGPAFHVLDANRPWCYMMVHPLALLDEALDDLENDIIDF 117
DB 1 MMEIORKQJLDYLMKGRQJLQPOSSLDANPWCYILHLSIALLGTVDELESNAIDF 60
QY 118 LARCODKDGYSGGPCQLPLHATFYAAVNTLVITIGSERALSSIRGNLYNMLQMKVSG 177
DB 61 LGRGQSGEGYGGGPGQLPLHATFYAAVNTLVITIGSERALSSIRGNLYNMLQMKVSG 120
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QY 178 AFRMHGGEIDVRASYTAISVSLVNTLDFEKLKGVGDYIARCQYEGGIAGEPYAEAHG 237
DB 121 GFRHDMGGEIDVRACYTAISVSLVNTLIMDELPFGGLDYLISCTYBGGIGGEPGSAHG 180
QY 238 GYTFPGALAILLNEAKVDLPISLIGVAVRQGYEGCGFQGRTKNLVYGCYSFMQAAIAF 297
DB 181 GYTYCGLAAMILNEVRLNMLSNMNAVHROGVEGFOGRTKNLVYGCYSFMQAAIAF 240
QY 298 TOKLITIVDQKASSYCKR-----PSGEDACSTSYSCFAKRS 336
DB 241 LQRLYSTNDHDVHGSSHISEGTNEHHNDEDEDDDDDDSDDEDNDESVNCHRIHHT 300
QY 337 SSAVDYAKFGFDFEQSNOIGPFLHNIALQYILLCQVLEGGLRDKRGRNRDHYHSCYC 396
DB 301 ST-----YINRMQL--VFDSLGLQRYVLCSKIPDGGRDKRPRPRDYHHCYC 348
QY 397 LSGLAVSQYSAMDYTGSCPLPQHVLAGFYSNLEPIHPLVNVLDLKYATPAIEFF 449
DB 349 LSGLSVAOHAWLKDEDPRPLTRDIMGYSNLEPFQDLHNIVMDQYNEAIEFF 401

RESULT 9
AAW97867 standard; Protein; 404 AA.
XX
AC AAW97867;
XX
DT 07-JUN-1999 (first entry)
XX
DE Arabidopsis farnesyl transferase.
XX
KW Farnesyl transferase; ERAl gene; transgenic plant;
KW stress tolerance; cold tolerance; drought tolerance;
KW salt tolerance; senescence.
XX
OS Arabidopsis thaliana.
XX
PN WC9906580-A2.
XX
PD 11-FEB-1999.
XX
PF 29-JUL-1998; 98WO-US15664.
XX
PR 01-AUG-1997; 97US-0054474.
XX
PA (PERF-) PERFORMANCE PLANTS INC.
XX
PI Bonetta D, Cutler S, Ghassemlan M, McCourt P;
DR WPI: 1999-153807/13.
DR N-PSDB: AAX24384.
XX
PT Now isolated Arabidopsis farnesyl transferase gene - used to develop
PT plants having improved stress tolerance, altered lateral branching,
PT delayed senescence or altered flowering numbers
XX
PS Claim 4; Fig 2; 66pp; English.
XX
CC This is the amino acid sequence of the farnesyl transferase (FT)
CC encoded by the ERAl gene (see AAX24384) of Arabidopsis thaliana. FT
CC is involved in the regulation of lateral branching, regulation of
CC the response to abscisic acid (ABA) and regulation of senescence.
CC A claimed nucleic acid construct comprises a promoter and a
CC nucleic acid encoding an inhibitor of a plant FT. Such constructs
CC can be used to produce plants having improved tolerance to drought,
CC salt and cold stress, reduced lateral branching, delayed senescence
CC and increased numbers of flowers. Also claimed in a seed, plant
CC part, cell or tissue culture or regenerated transgenic plant
CC containing the claimed nucleic acid construct, the plant being a
CC monocot or dicot, especially a Brassica sp. A plant having a
CC mutation in the ERAl gene that results in loss of FT activity is
CC also claimed.
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PR 30-OCT-1992; 92US-0968782.  
XX (MERI ) MERCK & CO INC.  
XX  
PI Diehl RE, Gibbs JB, Kohl NE, Omer CA:  
XX WPI; 1994-167373/20.  
DR N-PSDB; AAQ64886.  
XX  
XX Mammalian farnesyl protein transferase prodn. - used in assays  
PT for cpds, with inhibitory activity for the identification of  
PT anticancer agents  
XX  
XX  
PS Disclosure; Fig 1; 69pp; English.  
XX  
CC The cDNA encoding the bovine beta subunit of FPPase was isolated  
CC from a bovine brain oligo (dt) primed cDNA library in lambda gt10  
CC using a probe based on a fragment of the rat FPPase beta subunit.  
CC The FPPase can be used to isolate human FPPase sequences which can  
CC be used to assess the inhibitory activity of a cpd. In the  
CC farnesylation of a protein substrate. The assay can be used to  
CC identify anticancer agents.  
CC See also AAR54830-2.  
CC  
XX  
SQ Sequence 437 AA:  
  
Query Match 39.2%; Score 944.5; DB 15; Length 437;  
Best Local Similarity 43.3%; Pred. No. 9e-88;  
Matches 198; Conservative 62; Mismatches 138; Indels 59; Gaps 7;  
  
QY 5 POSTPPGDDPAAADDLR-----LTVOVEQMKYKARVDIYRSLFGAAPTGS 56  
DB 12 PPSPPSWSEPLSLRREHARELDDSVETVSIQAKYEEKIOEVFSY---KFNHLY 68  
XX  
XX  
QY 57 IMLEMRDQHIEYLTPLRHMGPAFHVLDANRPWLCYMWVHPALDLDDLENDIID 116  
DB 69 PRVLQREKHFHYLKRGLRQLTDAVECLDSRPWLCYWIHSLELDEPIPOKATVDCQ 128  
QY 117 FLARCDKDGSGGPGQPLRLATTYAANVTLVITIGSERALSSINRGNLYNFMLOKDV 176  
DB 129 FLELCQSPDGFGGPGQYPLAPTYAANVALLCIIGTEAVNINREKLLQYLSLKQPD 188  
QY 177 GAFRMHNGEIDVRASTATSVASLVNIDFKLAKGVDIYARQTEGGIAGEPYAEAH 236  
DB 189 GSFLMHNGEVDVRSACVASVSLTNIITPDLFEGTAEWIARQNMGGIGGVPMEAH 248  
QY 237 GGYTFGCLALILINAEKVDLPISLIGVAFRQ-GVECGFGQRTNKLVDGCSFMQCAAI 295  
DB 249 GGYTFGCLALILINAEKVDLPISLIGVAFRQ-GVECGFGQRTNKLVDGCSFMQAG-- 306  
QY 296 AFYQKLITIVDKLKSYSCKRPSGEDACTSYGCTAKKSSAVDYAKRGPDIQOSNQ 355  
DB 307 -----LPLRLRALHA-----QGDPLMSRW----- 328  
QY 356 IGRPLFNIALQOYILLCQVLEGLRDKPGKNRDHYHSCYCLGSLAVSOYSAMTDGSCP 415  
DB 329 ---MFHQALQDEYILMCCQCPRTGGLDKPKGSRDFTHTCCLSLGSLIAQHFG-----SGAM 381  
QY 416 LPOHVLGPTSNLEPIHPLIYNNVLDKYHTAYEFPSEE 452  
DB 382 LHDVVLGVPENALQPTHPYVNIQPDKIQTATHTFLQK 418  
  
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ID AAR49740 standard; Protein; 437 AA.  
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XX AAR49740;  
AC  
XX  
DT 08-AUG-1994 (first entry)  
XX  
DE Farnesyltransferase beta-subunit.  
XX

KW Farnesyltransferase; FT; beta-subunit; p21ras; ras protein;  
XX cancer therapy.  
XX  
XX Rattus sp.  
OS  
XX  
PN WO9404561-A.  
XX  
XX  
PD 03-MAR-1994.  
XX  
XX  
PF 24-AUG-1993; 93WO-0508062.  
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PR 24-AUG-1992; 92US-0935087.  
XX  
XX  
PA (GENTH ) GENENTECH INC.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Brown MS, Goldstein JL, Marsters JC, Reiss Y;  
XX  
XX WPI; 1994-083105/10.  
DR N-PSDB; AAQ43398.  
XX  
XX  
PT New farnesyl-transferase inhibitors - used for inhibiting  
PT attachment of a farnesyl moiety to a p21ras protein in malignant  
PT cells  
XX  
XX  
PS Disclosure; Page 120-23; 183pp; English.  
XX  
XX  
CC The cDNA (AAQ43398) and amino acid (AAR49740) sequences of rat  
CC farnesyltransferase (FT) beta-subunit FT were determined. The cDNA  
CC may be used to produce recombinant FT, useful for screening  
CC potential anticancer agents that prevent expression of p21ras.  
CC The beta-subunit conserved region is given in AAR49781.  
CC  
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DB 129 FLELCQSPDGFGGPGQYPLAPTYAANVALLCIIGTEAVNINREKLLQYLSLKQPD 188  
QY 177 GAFRMHNGEIDVRASTATSVASLVNIDFKLAKGVDIYARQTEGGIAGEPYAEAH 236  
DB 189 GSFLMHNGEVDVRSACVASVSLTNIITPDLFEGTAEWIARQNMGGIGGVPMEAH 248  
QY 237 GGYTFGCLALILINAEKVDLPISLIGVAFRQ-GVECGFGQRTNKLVDGCSFMQCAAI 295  
DB 249 GGYTFGCLALILINAEKVDLPISLIGVAFRQ-GVECGFGQRTNKLVDGCSFMQAG-- 306  
QY 296 AFYQKLITIVDKLKSYSCKRPSGEDACTSYGCTAKKSSAVDYAKRGPDIQOSNQ 355  
DB 307 -----LPLRLRALHA-----QGDPLMSRW----- 328  
QY 356 IGRPLFNIALQOYILLCQVLEGLRDKPGKNRDHYHSCYCLGSLAVSOYSAMTDGSCP 415  
DB 329 ---MFHQALQDEYILMCCQCPRTGGLDKPKGSRDFTHTCCLSLGSLIAQHFG-----SGAM 381  
QY 416 LPOHVLGPTSNLEPIHPLIYNNVLDKYHTAYEFPSEE 452  
DB 382 LHDVVLGVPENALQPTHPYVNIQPDKIQTATHTFLQK 418  
  
RESULT 13

ID	AAr77840	AAr77840 standard; Protein: 437 AA.
XX	AAr77840:	
XX	23-JAN-1996	(first entry)
XX	Rat	farnesyl protein transferase beta subunit.
XX	Farnesyl transferase;	inhibitor; cancer; ras; p21.
XX	Rattus sp.	
XX	US5420245-A.	
XX	30-MAY-1995.	
XX	18-APR-1990;	90US-0510706.
XX	16-JAN-1992;	92US-0822011.
XX	18-APR-1990;	90US-0510706.
XX	20-NOV-1990;	90US-0615715.
XX	03-APR-1992;	92US-0863169.
XX	(TEXA )	UNIT TEXAS.
XX	Brown MS,	Goldstein JL, Reiss Y;
XX	WPI; 1995-206308/27.	
XX	N-PSDB; A0094411.	
XX	New farnesyl transferase inhibitor peptide(s) - based on farnesyl	
XX	acceptor substrate carboxy terminal sequences, used for the	
XX	treatment of cancer	
XX	Example 3; Column 51-53; 55pp; English.	
XX	AAr77840 is the beta subunit of rat farnesyl transferase which	
XX	is involved in the farnesylation of various cellular proteins	
XX	including the cancer related ras proteins. It is used to produce the	
XX	complete farnesyl transferase molecule which is used to demonstrate	
XX	the effectiveness of peptide inhibitors capable of inhibiting	
XX	farnesyl transferases. The peptide inhibitors are useful for	
XX	treating cancers and ras-related cancers in particular.	
XX	Sequence 437 AA:	
XX	Query Match	39.1%; Score 942.5; DB 16; Length 437;
XX	Best Local Similarity	43.1%; Pred. No. 1.4e-87;
XX	Matches 197; Conservative	64; Mismatches 137; Indels 59; Gaps
XX	5 POSTPTGDDPAAADPDLP-----LTVGYEOMKVEARVGDYRSLFGAAPTMS	56
XX	12 PPSSEPWSSEPISLRPEHARERLDDSVETISTEQAVEKIOEVSSY--KFNHLV	68
XX	57 IMLELRDQHELYLPGLRHMGPAFVLDANRPWLCYMWVHPLALIDEALDDLENDIID	116
XX	69 PRLVLRREKHPIFLYLRGLRLTDARECDASRPWLCYWLHSLLELLEDEIPQIVATDVCQ	128
XX	117 FLARCDKDGCGSGPGGLPHLATTYAAVNTLVLTIGSERALSSINRGNLNFMLOMKDVS	176
XX	129 FLELCQSPDGCGGSGPGGYPHLAPTYAAVNALCIIGTEAVNVINREKLOYLSIKOPD	188
XX	177 GAFRMHDSGEIDVRAYSALYSASLVNLDLFKLAGVGDYIARCTQTEGGINGEPEYAEH	236
XX	189 GFLHNVGGEVDVRSAYCAASVSLNTITPDLFECTAEMWIRACQWEGGIGGVPMEMH	248
XX	237 GGYTCGTLAALLILNLEAEKVDLPDLIGWAFRQ-EGVECGFQGRTNKLVGCGSFMOGAI	295
XX	249 GGYTCGTLAALVILKKRSLNKLKSLLOMTSQMFEFGFGRCRKNLVDCGCSFMDAG--	306
XX	236 AFTQKLITIVDKOLKSLSCRRPSEEDACSTSSYCGCTAAKSSAAVDYAKFGDFIQOSNO	355

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Db      307  -----LRLPLRHALHA-----GQDDPALSMESH-----          328
Oy      356  IGPLFHNALDOYILLCSQVLEGLBDRPKNRDHYHSCYCLSGIAVSQYSMTDTGSCP 415
Db      329  ---MHOAOALDEYIIMCCOCPPAGGLDKPRKGRDYHHCYCISLSIAOHFG----SGAM 381
Oy      416  LPQHLYGYSNLLERIPHLNYNVLDKYNHTAYEFSEE 452
Db      382  LHDVVGVPENVLDPHTHPVYINIGPKVIQATTHFLQK 418

RESULT 14
AAW04428
ID      AAW04428 standard; Protein: 437 AA.
XX
AC      AAW04428;
XX
DF      30-JUL-1997 (first entry)
XX
DE      Rat farnesyl transferase enzyme beta subunit.
XX
KW      Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
KW      ras protein; K-ras B; malignant; detection; identification.
XX
OS      Rattus rattus.
XX
PN      MO9634113-A2.
XX
PD      31-OCT-1996.
XX
PF      29-APR-1996; 96WO-US05969.
XX
PR      27-APR-1995; 95US-0429964.
XX
PA      (TEXA ) UNIV TEXAS SYSTEM.
PI      Brown MS, Goldstein JL, James GL;
DR      WPI: 1996-497642/49.
DR      N-PSDB: AAT38709.
XX
PT      Assay for farnesyl transferase activity - by determining ability to
PT      transfer farnesyl moiety to K-Ras B protein, partic. useful for
PT      identifying inhibitors
XX
PS      Example 3; Page 143-147; 257pp; English.
XX
CC      AAW04428 shows the beta subunit of a farnesyl transferase (FT) enzyme
CC      derived from rat brain tissue. The enzyme was used in a method
CC      for identifying FT inhibitors. The method involved screening candidate
CC      compounds for the ability to inhibit the transfer of a farnesyl moiety
CC      to a K-ras B protein. FT inhibitors act by blocking the attachment of
CC      prenyl groups to ras proteins in malignant cells of patients suffering
CC      from cancer or precancerous states, and as such are used to treat such
CC      conditions.
SQ      Sequence 437 AA:

Query Match           39.1%; Score 942.5; DB 17; Length 437;
Best Local Similarity 43.1%; Pred. No. 1.4e-87;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps

Oy      5 POSTPTGGDDPAAADPDLP-----LTVOYEOVKVEARVDGIYSLRGCAAPTNS 56
Db      12 PSSSPVSWSEPLYSTRPEHAKRELDDDSYETSTIOAKEVERIDEVFSSY---KFNLV 68

Oy      57 IMLELMRDQHELEYTLPGLRHMGPFAFHVLDANRPWLCYVMVHPDLALDELDDLLENDI 116
Db      69 PRLVLAOREHHFYLRKGLRLTDATRECDASRWLCYTWILSHLELLEDDEIPQIVATDVQC 128

Oy      117 FLARCQKDQGTSGGPGQLPHLATTYYAAVNTLVTTGSERALLSINRGNIYNFMLOMKDVS 176
Db      129 FELTDCSPKGCGGPGGVPHLAPTYAAVNALCIITGEAEAVNINREKLQYLVSIKOPD 188

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 1, 2002, 18:07:56 ; Search time 19 Seconds  
(without alignments)  
581.072 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411  
Sequence: 1 MDPSFQSTRPPGDDPAAAD.....PLYNVLDKRYHTAYEFSEE 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCFUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	942.5	39.1	437	1 US-07-863-169A-3	Sequence 3, App11
2	942.5	39.1	437	2 US-08-429-964-3	Sequence 3, App11
3	942.5	39.1	437	3 US-07-935-087-3	Sequence 3, App11
4	942.5	39.1	437	4 PCT-US93-08062-3	Sequence 3, App11
5	940.5	39.0	437	5 US-08-424-268-10	Sequence 10, App1
6	940.5	39.0	437	6 PCT-US93-10442-10	Sequence 10, App1
7	940.5	39.0	819	7 US-08-424-268-20	Sequence 20, App1
8	940.5	39.0	819	8 PCT-US93-10442-20	Sequence 20, App1
9	939.5	39.0	437	9 US-08-424-268-6	Sequence 6, App11
10	939.5	39.0	437	10 PCT-US93-10442-6	Sequence 6, App11
11	931.5	38.6	444	11 US-07-935-087-7	Sequence 7, App11
12	898.5	37.3	387	12 US-07-863-169A-7	Sequence 7, App11
13	898.5	37.3	387	13 US-08-429-964-7	Sequence 7, App11
14	898.5	37.3	387	14 PCT-US93-08062-7	Sequence 7, App11
15	359	14.9	355	15 US-09-387-574-8	Sequence 8, App11
16	359	14.9	355	16 US-09-668-096-8	Sequence 8, App11
17	320	13.3	377	17 US-08-188-277B-4	Sequence 8, App11
18	320	13.3	377	18 US-08-429-964-78	Sequence 78, App1
19	313	13.0	377	19 US-08-188-277B-2	Sequence 78, App1
20	313	13.0	377	20 US-08-429-964-80	Sequence 80, App1
21	304.5	12.6	313	21 US-09-387-574-4	Sequence 4, App11
22	304.5	12.6	313	22 US-09-668-096-4	Sequence 4, App11
23	291.5	12.1	318	23 US-09-387-574-2	Sequence 2, App11
24	291.5	12.1	318	24 US-09-668-096-2	Sequence 2, App11
25	285	11.8	291	25 US-09-387-574-6	Sequence 6, App11
26	285	11.8	291	26 US-09-668-096-6	Sequence 6, App11
27	97	4.0	1090	27 US-09-346-237-5	Sequence 5, App11

28	96.5	4.0	2703	1 US-08-185-432-19	Sequence 19, App1
29	90	3.7	343	4 US-09-193-503B-1	Sequence 1, App1
30	90	3.7	579	2 US-08-864-224-11	Sequence 11, App1
31	90	3.7	781	4 US-09-193-503B-3	Sequence 3, App11
32	90	3.7	781	4 US-09-193-503B-6	Sequence 6, App11
33	90	3.7	781	4 US-09-193-503B-9	Sequence 9, App11
34	90	3.7	781	4 US-09-193-503B-11	Sequence 11, App1
35	89.5	3.7	334	3 US-08-883-526-4	Sequence 4, App11
36	89.5	3.7	979	3 US-08-690-473-2	Sequence 2, App11
37	86	3.6	1298	2 US-08-690-473-2	Sequence 2, App11
38	86	3.6	1298	4 US-09-259-821A-2	Sequence 2, App11
39	86	3.6	1298	4 US-08-843-659-2	Sequence 2, App11
40	84.5	3.5	558	4 US-09-148-680-2	Sequence 2, App11
41	84	3.5	334	3 US-09-120-365-64	Sequence 64, App1
42	84	3.5	334	4 US-09-515-039-64	Sequence 64, App1
43	83	3.4	461	4 US-09-122-210-2	Sequence 2, App11
44	83	3.4	461	4 US-09-443-681-2	Sequence 2, App11
45	82	3.4	3066	4 US-08-952-127-12	Sequence 12, App1

#### ALIGNMENTS

RESULT 1  
US-07-863-169A-3  
Sequence 3, Application US/07863169A  
Patent No. 5420245  
GENERAL INFORMATION:  
APPLICANT: Brown, Michael S.  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: Tetrapeptide-Based Inhibitors of Farnesyl  
TITLE OF INVENTION: Transferase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/863,169A  
FILING DATE: 03-APR-1992  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/822,011  
FILING DATE: 19-JAN-1992  
CLASSIFICATION: 530  
APPLICATION NUMBER: US 07/937,893  
FILING DATE: 18-APR-1991  
CLASSIFICATION: 530  
APPLICATION NUMBER: US 615,715  
FILING DATE: 20-NOV-1990  
CLASSIFICATION: 530  
APPLICATION NUMBER: US 510,706  
FILING DATE: 18-APR-1990  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:297/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-863-169A-3

Query Match 39.1%; Score 942.5; DB 1; Length 437;  
Best Local Similarity 43.1%; Pred. No. 2,8e-96;  
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADBDLPR-----LTVQVEOMKVEARVGDYRSIFGAAPTKS 56  
DB 12 PPSSPFWSEPLSLRREHARELQDDSVETVTSIEDAKKEIKOEYFSY---KENHLY 68  
QY 57 IMELMRDQHEIYLTPLRHMGRPAFHYLDANRPMLCYMWVHPALDLDEALDDLENDIID 116  
DB 69 PRVLQREKHFHYLKRGLRLQTLDAECLDASRPMLCYWLHSLLELDEPIQLVATDVQC 128  
QY 117 FLARCQKDGSGGPGQLPHLATTYAANVTLVTTIGSERLSSINGNLYNPMLOMKDVS 176  
DB 129 FLELCQSPDGGFGGPGQYHPLAPTYAANVALCIIGTEEAYNVINREKLLQYLYSLKOPD 188  
QY 177 GARFMDGGEIDYRASYTAISVSLVNIIDFLAKGVGYDIARQOTEGGIAGEPYAEAH 236  
DB 189 GSFLMHVGEVDYRSATCAASVASTNITITPDLFEGTAEMTARCOMWEGSIGVPGMEAH 248  
QY 237 GGYTFGGLAALLILNEAEKVDPSLIGWAFRO-GVECGFOGRTNKLVDGCSFMQAGAI 295  
DB 249 GGYTFGGLAALLILNEAEKVDPSLIGWAFRO-GVECGFOGRTNKLVDGCSFMQAG-- 306  
QY 296 AFQOKLITIVDKOLKSSYSCKRPSGEDACSTSSYCTAKKSSSAVDYAKGFPFIQSNQ 355  
DB 307 -----LLPLRLRALHA-----QGDPALSMSHW----- 328  
QY 356 IGPLFHNIALQOYIILCSQVLEGLRDKPGKNRDYHSCYCLSGLAVSQYSAMTDGSCP 415  
DB 329 ---MFIQOALQEIYILMCCQCPAGGLDKPKSKRDFHTCYCLSGLSIAQHFQ----SGAM 381  
QY 416 LPOHVLGPPYNSLLEPIHPLYNVLDKHYTAEPFSEE 452  
DB 382 LHDVVMGVPENVLQPHHYVNIIGDPKVIQATTFHFLQK 418

## RESULT 2

US-08-429-964-3  
Sequence 3, Application US/08429964  
Patent No. 5962243  
GENERAL INFORMATION:  
APPLICANT: BROWN, MICHAEL S.  
APPLICANT: GOLDSTEIN, JOSEPH L.  
APPLICANT: REISS, YUVAL  
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
TITLE OF INVENTION: TRANSFERASE INHIBITORS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-08/429,964  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,625

FILING DATE: 16-FEB-1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/822,011  
FILING DATE: ABANDONED  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US/91/02650  
FILING DATE: 18-APR-1991  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/615,715  
FILING DATE: 20-NOV-1990  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/510,706  
FILING DATE: 18-APR-1990 (ABANDONED)  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PARKER, DAVID L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:432/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 437 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-429-964-3

Query Match 39.1%; Score 942.5; DB 2; Length 437;  
Best Local Similarity 43.1%; Pred. No. 2,8e-96;  
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADBDLPR-----LTVQVEOMKVEARVGDYRSIFGAAPTKS 56  
DB 12 PPSSPFWSEPLSLRREHARELQDDSVETVTSIEDAKKEIKOEYFSY---KENHLY 68  
QY 57 IMELMRDQHEIYLTPLRHMGRPAFHYLDANRPMLCYMWVHPALDLDEALDDLENDIID 116  
DB 69 PRVLQREKHFHYLKRGLRLQTLDAECLDASRPMLCYWLHSLLELDEPIQLVATDVQC 128  
QY 117 FLARCQKDGSGGPGQLPHLATTYAANVTLVTTIGSERLSSINGNLYNPMLOMKDVS 176  
DB 129 FLELCQSPDGGFGGPGQYHPLAPTYAANVALCIIGTEEAYNVINREKLLQYLYSLKOPD 188  
QY 177 GARFMDGGEIDYRASYTAISVSLVNIIDFLAKGVGYDIARQOTEGGIAGEPYAEAH 236  
DB 189 GSFLMHVGEVDYRSATCAASVASTNITITPDLFEGTAEMTARCOMWEGSIGVPGMEAH 248  
QY 237 GGYTFGGLAALLILNEAEKVDPSLIGWAFRO-GVECGFOGRTNKLVDGCSFMQAGAI 295  
DB 249 GGYTFGGLAALLILNEAEKVDPSLIGWAFRO-GVECGFOGRTNKLVDGCSFMQAG-- 306  
QY 296 AFQOKLITIVDKOLKSSYSCKRPSGEDACSTSSYCTAKKSSSAVDYAKGFPFIQSNQ 355  
DB 307 -----LLPLRLRALHA-----QGDPALSMSHW----- 328  
QY 356 IGPLFHNIALQOYIILCSQVLEGLRDKPGKNRDYHSCYCLSGLAVSQYSAMTDGSCP 415  
DB 329 ---MFIQOALQEIYILMCCQCPAGGLDKPKSKRDFHTCYCLSGLSIAQHFQ----SGAM 381  
QY 416 LPOHVLGPPYNSLLEPIHPLYNVLDKHYTAEPFSEE 452  
DB 382 LHDVVMGVPENVLQPHHYVNIIGDPKVIQATTFHFLQK 418

## RESULT 3

US-07-935-087-3  
Sequence 3, Application US/07935087  
Patent No. 6083917  
GENERAL INFORMATION:  
APPLICANT: BROWN, MICHAEL S.

```

1  APPLICANT: GOLDSTEIN, JOSEPH L.
2  APPLICANT: REISS, YUVAL
3  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
4  TITLE OF INVENTION: THE IDENTIFICATION,
5  TITLE OF INVENTION: CHARACTERIZATION,
6  TITLE OF INVENTION: AND INHIBITION OF FARNESYL
7  TITLE OF INVENTION: PROTEIN TRANSFERASE
8  NUMBER OF SEQUENCES: 8
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: ARNOLD, WHITE & DUKKEE
11 STREET: P.O. BOX 4433
12 CITY: HOUSTON
13 STATE: TEXAS
14 COUNTRY: USA
15 ZIP: 77210
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: FLOPPY DISK
19 COMPUTER: IBM PC COMPATIBLE
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)
22 CURRENT APPLICATION DATA:
23 FILING DATE: 19920824
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US/07/822,011
27 FILING DATE: 01/16/92
28 ATTORNEY/AGENT INFORMATION:
29 NAME: PARKER, DAVID L.
30 REGISTRATION NUMBER: 32,165
31 REFERENCE/DOCKET NUMBER: UTSD:269/PAR
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 512-320-7200
34 TELEFAX: 512-474-7577
35
36 TELEX:
37
38 INFORMATION FOR SEQ ID NO: 3:
39
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 437 amino acid residues
42 TYPE: amino acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45
46 US-07-935-087-3
47
48
49 Query Match 39.1%; Score 942.5; DB 3; Length 437;
50 Best Local Similarity 43.1%; Pred No.2.8e-96;
51 Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps
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[illegible]

Db 129 FLELCSPDGGFGGPGQYTHLAFTAAVNAALCTIGTEEAIVNINREKLLQYLSLKOPD 188  
QY 177 GAFRMDGGEIDVASYTAISVASLVNILDPKLAKGVGYIARCQYEGGIAGEPYAEAH 236  
Db 189 GSFLLMHVGEVDVRSACASVASLTNITLPDLEFGTAEMIARQNMEGGICGVPGEAH 248  
QY 237 GGTFFCGLAALLINENKVDLPGLGWAFRQ-GVBCGQGRNTKLVDCYSFMOGAAI 295  
Db 249 GGTFFCGLAALLVILKRRSLNLSLQWVTSRQMRFGGRCNKLVDCYSFMOAG-- 306  
QY 296 AFTQKLTIVDKOLKSSYSCRRPGEACSTSSYGCYAKKSSAVDYAKFGPDFIQOSNQ 355  
Db 307 -----LLPLHRLAHLA-----QGDPALSMSHW----- 328  
QY 356 IGPLFNHIALQOYIILCSQYLEGLRDKPGKNDHYHSCYCLSGLAVSQYSAMTDTGSCP 415  
Db 329 ---MFHQALQOEVYILMCCQCPAGGLDLPKGSNDYFTYTCYCLSGLSIAQHFG----SGAM 381  
QY 416 LPOHVLGPRYSLNLEPIHPLNVVLQKHTYAEFFSEE 452  
Db 382 LHDVVLGVPENALQPTHVYVNIQDPKVIQATYTFLOK 418

## RESULT 5

US-08-424-268-10  
; Sequence 10, Application US/08424268  
; Patent No. 5821118  
; GENERAL INFORMATION:  
; APPLICANT: Omer, Charles A  
; APPLICANT: Diehl, Ronald E  
; APPLICANT: Gibbs, Jackson B  
; APPLICANT: Kohl, Nancy E  
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: United States of America  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Power Mac  
; OPERATING SYSTEM: System 7.5.3  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,268  
; FILING DATE: 4/24/95  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mulhard, David A  
; REGISTRATION NUMBER: 35,297  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)594-3903  
; TELEFAX: (908)594-4720  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 437 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; FRAGMENT TYPE: N-terminal  
; US-08-424-268-10

Query Match 39.0%; Score 940.5; DB 2; Length 437;  
Best Local Similarity 43.1%; Pred. No. 4.7e-96;  
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADBDLPR-----LTVQVEQMKVEARNGDIYNSLFGAAPTNS 56  
Db 12 PESSPWSEPLYSLRREHARERLQDDSVETVSIQDAKVEEKIOEYSSY---KENHLV 68  
QY 57 IMELMRDQHIETVLPGLRMRGPAFHVLDANRWMCLYWMHPLALLDEALDDLENDIID 116  
Db 69 PRLVLOREKHFNHLYLRLQRLTDVIECLDSRPMCLYWLHLSLELDEPTPOIVAVDVCQ 128  
QY 117 FLARCDKDCGSGPGCOLHLATTYAAVNTLVITIGSERALSSINGNLYNFMLOKMDVS 176  
Db 129 FLELCSPREGFGGPGQYTHLAFTAAVNAALCTIGTEEAIVNINREKLLQYLSLKOPD 188  
QY 177 GAFRMDGGEIDVASYTAISVASLVNILDPKLAKGVGYIARCQYEGGIAGEPYAEAH 236  
Db 189 GSFLLMHVGEVDVRSACASVASLTNITLPDLEFGTAEMIARQNMEGGICGVPGEAH 248  
QY 237 GGTFFCGLAALLINENKVDLPGLGWAFRQ-GVBCGQGRNTKLVDCYSFMOGAAI 295  
Db 249 GGTFFCGLAALLVILKRRSLNLSLQWVTSRQMRFGGRCNKLVDCYSFMOAG-- 306  
QY 296 AFTQKLTIVDKOLKSSYSCRRPGEACSTSSYGCYAKKSSAVDYAKFGPDFIQOSNQ 355  
Db 307 -----LLPLHRLAHLA-----QGDPALSMSHW----- 328  
QY 356 IGPLFNHIALQOYIILCSQYLEGLRDKPGKNDHYHSCYCLSGLAVSQYSAMTDTGSCP 415  
Db 329 ---MFHQALQOEVYILMCCQCPAGGLDLPKGSNDYFTYTCYCLSGLSIAQHFG----SGAM 381  
QY 416 LPOHVLGPRYSLNLEPIHPLNVVLQKHTYAEFFSEE 452  
Db 382 LHDVVLGVPENALQPTHVYVNIQDPKVIQATYTFLOK 418

## RESULT 6

PCT-US93-10442-10  
; Sequence 10, Application PC/TUS9310442  
; GENERAL INFORMATION:  
; APPLICANT: Omer, Charles A  
; APPLICANT: Diehl, Ronald E  
; APPLICANT: Gibbs, Jackson B  
; APPLICANT: Kohl, Nancy E  
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: United States of America  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/10442  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/968,782  
; FILING DATE: 10/30/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mulhard, David A  
; REGISTRATION NUMBER: 35,297  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)594-3903  
; TELEFAX: (908)594-4720  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 437 amino acids  
; TYPE: amino acid



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10442  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/968,782  
FILING DATE: 10/30/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Muthard, David A  
REGISTRATION NUMBER: 35,297  
REFERENCE/DOCKET NUMBER: 18858  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)594-3903  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 819 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEtical: NO  
FRAGMENT TYPE: N-terminal  
PCT-US93-10442-20

Query Match 39.0%; Score 940.5; DB 5; Length 819;  
Best Local Similarity 43.1%; Pred. No. 1.3e-95;  
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADDDLR-----LTVQVEQMKYEAAGVYDIYRSLFGAAPTGS 56  
DB 12 PSSSPWSEPLYSLRREHARELRQDDSVETVTSIEQAKVEKIQEYFSY---KFNHLY 68  
QY 57 IMELMRDQHEVLTPLGRHMGPAFHVLDANRPMCYMWVNPALLDEALDDLENDIID 116  
DB 69 PRLVQREKHNHLYLKRGLQTDAYECLDASRPMCYWILHSLLELDEPIRQIVATDVQC 128  
QY 117 FLARCQDKGCGYSGGPGQLPHLATTYAANVTLYTIGSERALSSINRGNLYNFMLOMKDVS 176  
DB 129 FLELCQSPREGFGGPGQYPHLAPTYAANVALCIGTEEAADIINREKLLQYLSLKQPD 188  
QY 177 GAFMMDGGEIDVRASTAIASVSLVNLDFKLAKGVGDYIARCQYEGTAGEPYAEAH 236  
DB 189 GSFMLHNGEVDYRSACASVASLTNITPDLFEGTAEMTARCONNEGIGVPGMEAH 248  
QY 237 GGYTFGCGLAALILNEAEKVDLPGLGMVAFRQ-GVECGFGGRTNKLVDGCSFMQGAII 295  
DB 249 GGYTFGCGLAALVILKRERSLMLKSLQWVYSRQMRFGGFGRCNKLVDGCSFMQAG-- 306  
QY 296 AFTOKLITVDKOLKSSYCKRPSGEDACSTSYGCTAKKSSAVDYAKFGFDTIOQSNQ 355  
DB 307 -----LPLRLRALHA-----QGDPAISMSPW----- 328  
QY 356 IGPLFHNIALQYIILCSOVLGGLRDKPGKNDHYHSCYCLSGLAVSQYSAMTDGSCP 415  
DB 329 ---MFHQALQDEYILMCCQCPGGLDKPKGRSDYHTCYCLSLGSLIAOHFG-----SGAM 381  
QY 416 LPOHVLGPNLSLEPIHPLVNVLDKYHTAYEEFSEE 452  
DB 382 LHDVVLGVPENALQPTHTPVYINIGPKVIAQTTFVLQK 418

RESULT 9  
US-08-424-268-6  
Sequence 6, Application US/08424268  
Patent No. 582118  
GENERAL INFORMATION:  
APPLICANT: Omer, Charles A  
APPLICANT: Diehl, Ronald E  
APPLICANT: Gibbs, Jackson B

APPLICANT: Kohl, Nancy E  
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein  
TRANSFERASE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Power Mac  
OPERATING SYSTEM: System 7.5.3  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,268  
FILING DATE: 4/24/95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muthard, David A  
REGISTRATION NUMBER: 35,297  
REFERENCE/DOCKET NUMBER: 18858PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)594-3903  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 437 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEtical: NO  
FRAGMENT TYPE: N-terminal  
US-08-424-268-6

Query Match 39.0%; Score 939.5; DB 2; Length 437;  
Best Local Similarity 43.1%; Pred. No. 6e-96;  
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADDDLR-----LTVQVEQMKYEAAGVYDIYRSLFGAAPTGS 56  
DB 12 PSSSPWSEPLYSLRREHARELRQDDSVETVTSIEQAKVEKIQEYFSY---KFNHLY 68  
QY 57 IMELMRDQHEVLTPLGRHMGPAFHVLDANRPMCYMWVNPALLDEALDDLENDIID 116  
DB 69 PRLVQREKHNHLYLKRGLQTDAYECLDASRPMCYWILHSLLELDEPIRQIVATDVQC 128  
QY 117 FLARCQDKGCGYSGGPGQLPHLATTYAANVTLYTIGSERALSSINRGNLYNFMLOMKDVS 176  
DB 129 FLELCQSPREGFGGPGQYPHLAPTYAANVALCIGTEEAADIINREKLLQYLSLKQPD 188  
QY 177 GAFMMDGGEIDVRASTAIASVSLVNLDFKLAKGVGDYIARCQYEGTAGEPYAEAH 236  
DB 189 GSFMLHNGEVDYRSACASVASLTNITPDLFEGTAEMTARCONNEGIGVPGMEAH 248  
QY 237 GGYTFGCGLAALILNEAEKVDLPGLGMVAFRQ-GVECGFGGRTNKLVDGCSFMQGAII 295  
DB 249 GGYTFGCGLAALVILKRERSLMLKSLQWVYSRQMRFGGFGRCNKLVDGCSFMQAG-- 306  
QY 296 AFTOKLITVDKOLKSSYCKRPSGEDACSTSYGCTAKKSSAVDYAKFGFDTIOQSNQ 355  
DB 307 -----LPLRLRALHA-----QGDPAISMSPW----- 328  
QY 356 IGPLFHNIALQYIILCSOVLGGLRDKPGKNDHYHSCYCLSGLAVSQYSAMTDGSCP 415  
DB 329 ---MFHQALQDEYILMCCQCPGGLDKPKGRSDYHTCYCLSLGSLIAOHFG-----SGAM 381  
QY 416 LPOHVLGPNLSLEPIHPLVNVLDKYHTAYEEFSEE 452  
DB 382 LHDVVLGVPENALQPTHTPVYINIGPKVIAQTTFVLQK 418



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Db      129 FLELQSPGEGGCGPGQYPHLAPFYAAVNMALCIITGEAVDIIINRELLQYLKSLQPD 188
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Oy      177 CAFRHHOGGELIDVRASTYAIVASLVNLTDFKLAKGCDYIARCQTYEGCIAGEPYAEAH 238
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      189 GSFLLHWGGEVDVRSAYCAASVASTLTNTITPDEFEGETAEWTAIRCQNNEGGIGGPGMEAH 248
Oy      237 GGYTFCGTAALILLINEAKVLDPLSLIGVAVRQ--GVEGCGGPRNTKLYDVCYSWQCAAI 299
      |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      249 GGYTFCGTAALILKREBSLMLKSLQWVSRQRHFEQGFQGRCKNLVDGYSFWQAG-- 306
Oy      296 AFTOKLITIVDKOLKSSYSCKRPSGDEACSTSYSGCTAKKSSAVDYAKFGDFETIQSNQ 355
      ||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      307 -----LRLHLRALHA-----QQDPAKLSMHW----- 328
Oy      336 IGRFLFNIALQOYIILCSQVLEGGELRDKPGKNRDHYHSCYCLSGLAVSQYSAMTDITGSCP 415
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      329 ---MFHQOALOEYILCMCHCPAGGLDRPGKSRPFHTCYCLSGLSIAQHFG-----SGAM 381
Oy      416 LPHQVLYGSYNLEPIHPLVNVVLDKTYTAEFSSSE 452
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      382 LHDVVLGVPENALQPTHPVNIIGPKYIQVTTYFLQK 418

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:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 387 amino acids
:      TYPE: amino acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
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US-07-863-169A-7

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: FILING DATE: ABANDONED
: CLASSIFICATION: 435
: APPLICATION NUMBER: PCT/US/91/02650
: FILING DATE: 18-APR-1991
: CLASSIFICATION: 435
: APPLICATION NUMBER: US 07/615,715
: FILING DATE: 20-NOV-1990
: CLASSIFICATION: 435
: APPLICATION NUMBER: US 07/510,706
: FILING DATE: 18-APR-1990 (ABANDONED)
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: PARKER, DAVID L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: UTSD:432/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (713) 789-2679
: TELETYPE: 79-0924
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 387 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-429-964-7

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Query Match          37.3%; Score 898.5; DB 2; Length 387;
Best Local Similarity 44.3%; Pred. No. 1.8e-91;
Matches 185; Conservative 58; Mismatches 124; Indels 51; Gaps 6;

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QY 36 VEARVGDYRSLSFGAAPTNTKSLMELEMRDOHIEYLPGLRHMGPAHFVLDANRPWLCTYWM 95
DB 1 VEEKIOEVFSSY--KENHLVPRVLVQREKHFFYLKRGRLTDAYECILDASHPWLCTYWI 57
QY 96 VHPFLALDELDDDDLENDIIDFLARCDKDGYSGGGPGOLPHLATYTAANTLVTTGSR 155
DB 58 LHSLELLDEPIPOIVATDVQCFLCQSPGCGGGGPGQPHLAPTYAAVNALCIIIGTEE 117
QY 156 ALSISNGNLNFMLOKMDVSAFRMHGGEIDVRASYTAISVASYNIIDFLAKVGVD 215
DB 118 AYDIINREKLYLTLKQDGSFLMHVGEVDVRSAYCAVASLNIITPDLFEGTAE 177
QY 216 YIARCQTEGGIAGEPYAEAHGGYTCGGLAALLLNEAEVVDPSLIGWAFRGV-ECG 274
DB 178 WIRACQWMEGGIGVPGMEAHGGYTCGGLAALLYLKRESLNLKSLQWVTSRQMLFEGG 237
QY 275 FQGRTKLVGCGYSFWOGAALIAFTOKLITVDKOLKSSYCKRPSGSDACSTSSYGTAK 334
DB 238 FQGRCKNLVDGCTSFOWAG-----LLPLLRALHA-----QGDPLSMNSHW----- 278
QY 335 KSSSAVDYAFGDFDIQOSNQIGPLFHNIALQOYIILCSQVLEGLDKRGNRDHYHSC 394
DB 279 -----MFIQALQOYIILMCCOCPRAGGLDKRCKSRDFTHTC 314
QY 395 YCLSGIAVSOYAMTDGSCPLDPQHVLGPSNLEPIHPLYNVLDKYHTAYEFSEE 452
DB 315 YCLSGLSIAQHFG-----SGAMLDHVVLGVPENALQPTHPYVNIIGPRKVIQATTYFLQK 368

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RESULT 14
PCT-US93-08062-7
: Sequence 7, Application PC/TUS9308062
: GENERAL INFORMATION:
: APPLICANT:
: SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
: SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
: SEQUENCE CHARACTERISTICS: REISS, YUVAL
: SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
: ADDRESSEE: METHODS AND COMPOSITIONS FOR
: ADDRESSEE: THE IDENTIFICATION,
: ADDRESSEE: CHARACTERIZATION AND

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: ADDRESSEE: INHIBITION OF
: ADDRESSEE: FARNESYLTRANSFERASE
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ARNOLD, WHITE & DURKEE
: STREET: P.O. BOX 4433
: CITY: HOUSTON
: STATE: TEXAS
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK/ASKII
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORDPERECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/08062
: FILING DATE: AUGUST 24, 1993
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/935,087
: FILING DATE: 24 AUGUST 1992 (24.08.92)
: NAME: UNKNOWN
: ATTORNEY/AGENT INFORMATION:
: NAME: PARKER, DAVID L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: UTEFD377PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-320-7200
: TELEFAX: 512-474-7577
: TELETYPE: NOT AVAILABLE
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 387 amino acid residues
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
PCT-US93-08062-7

```

```

Query Match          37.3%; Score 898.5; DB 5; Length 387;
Best Local Similarity 44.3%; Pred. No. 1.8e-91;
Matches 185; Conservative 58; Mismatches 124; Indels 51; Gaps 6;

```

```

QY 36 VEARVGDYRSLSFGAAPTNTKSLMELEMRDOHIEYLPGLRHMGPAHFVLDANRPWLCTYWM 95
DB 1 VEEKIOEVFSSY--KENHLVPRVLVQREKHFFYLKRGRLTDAYECILDASHPWLCTYWI 57
QY 96 VHPFLALDELDDDDLENDIIDFLARCDKDGYSGGGPGOLPHLATYTAANTLVTTGSR 155
DB 58 LHSLELLDEPIPOIVATDVQCFLCQSPGCGGGGPGQPHLAPTYAAVNALCIIIGTEE 117
QY 156 ALSISNGNLNFMLOKMDVSAFRMHGGEIDVRASYTAISVASYNIIDFLAKVGVD 215
DB 118 AYDIINREKLYLTLKQDGSFLMHVGEVDVRSAYCAVASLNIITPDLFEGTAE 177
QY 216 YIARCQTEGGIAGEPYAEAHGGYTCGGLAALLLNEAEVVDPSLIGWAFRGV-ECG 274
DB 178 WIRACQWMEGGIGVPGMEAHGGYTCGGLAALLYLKRESLNLKSLQWVTSRQMLFEGG 237
QY 275 FQGRTKLVGCGYSFWOGAALIAFTOKLITVDKOLKSSYCKRPSGSDACSTSSYGTAK 334
DB 238 FQGRCKNLVDGCTSFOWAG-----LLPLLRALHA-----QGDPLSMNSHW----- 278
QY 335 KSSSAVDYAFGDFDIQOSNQIGPLFHNIALQOYIILCSQVLEGLDKRGNRDHYHSC 394
DB 279 -----MFIQALQOYIILMCCOCPRAGGLDKRCKSRDFTHTC 314
QY 395 YCLSGIAVSOYAMTDGSCPLDPQHVLGPSNLEPIHPLYNVLDKYHTAYEFSEE 452
DB 315 YCLSGLSIAQHFG-----SGAMLDHVVLGVPENALQPTHPYVNIIGPRKVIQATTYFLQK 368

```

```

RESULT 15

```

```

US-09-387-574-8
; Sequence 8, Application US/09387574
; Patent No. 6168951
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Kinney, Tony
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Geranylgeranyl Transferases
; FILE REFERENCE: BB-1239
; CURRENT APPLICATION NUMBER: US/09/387,574
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: 60/098,743
; EARLIER FILING DATE: September 1, 1998
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 355
; TYPE: PRF
; ORGANISM: Glycine max
US-09-387-574-8

```

Query Match 14.9%; Score 359; DB 4; Length 355;

Best Local Similarity 27.3%; Pred. No. 2.3e-31; Matches 104; Conservative 58; Mismatches 125; Indels 94; Gaps 11;

```

QY 63 RDQIEVLPGLRMGPAFHVLDANRPMLCYMWVHPLALD---EALDDLENDIIDFLA 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 17 KDVAHTLELMYVLLPSYEQEINHLTLAFVYISGLDILDSLHKVAKDAVSWVLSFOA 76
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 120 RCOOK---DCYSGGPG---QLP-----HLATYAANVTLYTIGSERALSS 159
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 77 HPGAKTDLNCGQFGFGHSGKTSQFPDPDENGVLINNSHLASTYCAISLTKVYE--LSN 134
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 160 INRGNLYNFMLOMKDVSGAF-RMHGGEIDYRASATAISVASLVNILDFKLAKGVGYIA 218
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 135 LDSEITVTSNRNLQPPGSPFIPHTGETDLRFVYCAALICFMDNWSGMOKEKTDYIL 194
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 219 RCOTYEGGIAEPTAEAHGCTTFCGLAALLINEAEK-----VDLPSLIGVAF 267
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 195 RCQSYDGCFCGLVPGAESHGATYCAMASLRMGFIEDNILLSCASSSLIDAPLLDWILQ 254
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 268 RQVCEGFGQRTNKLIVGCVSFMQAAIAFTQKLITVDKQLKSSYCKRPSGEDACSTS 327
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 255 RQGTIDGFGQRPKNSSDTCTAFWIGAVL-----RILG----- 286
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 328 SYGCTAKSSAVDYAKFGFDFIQSNQIGPLFHNIALQOYIILCSQVLEGLRDKPKGN 387
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 -----GKFFVD-----NKLARGFLLSG-QYKYGGSFKFPGEY 317
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 388 RDIHSCYCLSGLAVSQYSAM 408
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 318 PDLVHSYGGFTAFSLIESGL 338
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: November 1, 2002, 18:15:42  
Job time : 23 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 17:58:05 ; Search time 39 Seconds

(without alignments)  
1113.651 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411  
Sequence: 1 MDPSQSTPPPTGDDPAAMAAD.....PLYNVLDKRYHAYEFFSEE 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1357.5	56.3	470	2 T07673	farnesyltransferase
2	1353.5	56.1	470	2 T07605	protein farnesyltr
3	1315.5	54.6	419	2 JQ2254	farnesyl-diphospha
4	942.5	39.1	437	2 A40037	protein farnesyltr
5	940.5	39.0	437	2 B49274	protein farnesyltr
6	939.5	39.0	437	2 C49274	protein farnesyltr
7	805.5	33.4	401	2 T21291	hypothetical prote
8	623.5	25.9	382	2 T37836	probable protein f
9	618.5	25.7	431	1 BVBYP	geranylgeranyl-dip
10	342.5	14.2	375	2 T00565	geranylgeranyl-dip
11	327.5	13.6	311	2 S65091	geranylgeranyltran
12	326	13.5	325	2 S59834	probable protein p
13	320	13.3	377	2 A53044	geranylgeranyl-dip
14	313	13.0	377	2 B53044	geranylgeranyl-dip
15	297.5	12.3	355	2 T15296	hypothetical prote
16	289.5	12.0	355	2 S41686	geranylgeranyltran
17	282	11.7	331	2 B45977	Rab geranylgeranyl
18	279	11.6	331	2 G02431	geranylgeranyl tra
19	278	11.5	339	2 JC6177	geranylgeranyl-dip
20	275.5	11.4	304	2 I49116	geranylgeranyl tra
21	244.5	10.1	360	2 T27022	hypothetical prote
22	190.5	7.9	376	1 RGBY43	cell division cont
23	97	4.0	1090	2 S11823	alpha-dextrin endo
24	96.5	4.0	2703	1 A24420	notch protein - fr
25	95.5	4.0	705	2 A41322	N-acetylmuramoyl-L
26	93.5	3.9	2512	2 E70751	probable ntp prote
27	92.5	3.8	346	2 A70590	hypothetical prote
28	91.5	3.8	791	2 T42691	hypothetical prote
29	90.5	3.8	271	2 F69442	hypothetical prote

30	90	3.7	343	1 RGBP1	recombinase - phag
31	90	3.7	350	2 JC7213	Cre recombinase pr
32	90	3.7	608	2 T34994	probable long-chain
33	90	3.7	1039	2 C84745	hypothetical prote
34	90	3.7	2895	2 H85362	hypothetical prote
35	89.5	3.7	334	2 A58195	caldesmon L (EC 3.
36	89.5	3.7	704	2 T03478	probable DNA-direc
37	89.5	3.7	1025	2 T45647	receptor protein k
38	89	3.7	1432	2 E71624	rikin PEB0055c - m
39	89	3.7	1316	2 T14895	DNA helicase 1 - A
40	88.5	3.7	2155	2 T30197	alpha tectorin - m
41	88	3.6	281	2 G87451	hypothetical prote
42	88	3.6	361	2 G89916	hypothetical prote
43	88	3.6	1214	2 G70953	probable suca prot
44	87.5	3.6	404	2 A84211	hypothetical prote
45	87.5	3.6	765	2 H84247	adaptive-response

#### ALIGNMENTS

RESULT 1					
T07673	farnesyltransferase (EC 2.5.1.29) chain B - tomato				
C:Species: Lycopersicon esculentum (tomato)					
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000					
C:Accession: T07673					
R:Valovsky, S.: Trueblood, C.E.; Gallian, K.L.; Narita, J.O.; Jenkins, S.M.; Rine, J.; Mol. Cell. Biol. 17, 1986-1994, 1997					
A:Title: Plant farnesyltransferase can restore yeast ras signaling and mating.					
A:Reference number: Z07721; M01D:97219988					
A:Accession: T07673					
A>Status: preliminary; translated from GB/EMBL/DBJ					
A:Molecule type: mRNA					
A:Residues: 1-470 <YAL>					
A:Cross-references: EMBL:083708; NID:q1815667; PIDD:AA049666.1; PID:q1815668					
A:Experimental source: cultivar VENT Cherry LA1221					
A:Note: farnesylates proteins					
C:Gene(s):					
A:Gene: FMB					
C:Superfamily: DPRL protein					
C:Keywords: heterodimer; transferase					
Query Match	56.3%	Score 1357.5;	DB 2;	Length 470;	
Best Local Similarity	57.3%	Pred. No. 4.8e-108;			
Matches 256;	Conservative 68;	Mismatches 100;	Indels 23;	Gaps 3;	
QY	25	RLTVTOEOMKVEARVGDYRSLFGAAPNPKSIMLELRDHOHLEYLPGRHMGPAFHYL	84		
DB	5	KVITLEDQWVERRVEIYDFYISIPNSPSDLITERDNHGYLSQGLKLPSPSVL	64		
QY	85	DANRPMILCYMMVHPPLALDEALDDLENDIIDFLARCQDKGSGGPGQLPHLATYYAA	144		
DB	65	DASRPMILCYMTLHSLALGSGIGKLENDIIDFLTRQDQDKGSGGPGQPHLATYYAA	124		
QY	145	VNLTVTIGSERALSSINRGUNYFMLOMKDYSCAFRHHGGEIDVRSYTAISVASLVNI	204		
DB	125	VNSLTITGKPEALSSINREKLYPLRMKDAISGCFRHHGGEIDVRSYTAISVASLVNI	184		
QY	205	IDPFLAGVDGYIARCTQYGGGIGGEYAEAGGYTCGLAALLLMEAEKVDLPSTLIGW	264		
DB	185	VDDLELNGVGNVYILSCQTYEGINGEPSEAHGGYTCGLAALLLMEAEKVDLPSTLIGW	244		
QY	265	VAFRQYEGCFQGRNTKLVDCYSFMOGAAIAFTOKLITTVDKOLKSSYCKRRSGEDAC	324		
DB	245	VVFRQYEGGFGQGRNTKLVDCYSFMOGAAVFLQRLNLIVHBDGLSNDLSTESADSS	304		
QY	325	ST-----SST-----GCTAKKSSSVDYAKRGFDPIQSNQIGPLPHN	362		
DB	305	ESELDEEHELEGISSHVODTFPLGAGACQACQENASHSPKTIADTCYERINPRIPAFDS	364		
QY	363	IALQOYVLLCSQVLEGGLRQKPKGNRHHYSCYCLSLAVSAYSAMMDTSSCLPQVILG	422		

Dh 365 MYLQOYVLLCSQIEVCGRDKPGKGRDYHHCYCLSGLSIAQYSWTDEADSTPLPRDVF 424

Oy 423 PYSN-LLEPIHPLNVLDKHTAYEF 448

Db 425 PYSKCLLEQVHPLFNVLDRYEAAREY 451

## RESULT 2

T07605

protein farnesyltransferase (EC 2.5.1.-) beta chain - tomato

C:Species: Lycopersicon esculentum (tomato)

C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-May-2000

C:Accession: T07605

R:Kadachouk, D.; Narita, J.O.

Plant Mol. Biol. 34, 831-835, 1997

A:Title: Foldback transposable elements in plants.

A:Reference number: 216045; MUID:97422406

A:Accession: T07605

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-470 <REB>

A:Cross-references: EMBL:U75644; NID:92182814; PIDN:AAB69757.1; PID:92182815

A:Experimental source: strain VENT Cherry

C:Genetics:

A:Gene: FTR

A:Insertions: 38/2; 67/2; 102/3; 114/3; 142/2; 160/2; 177/3; 199/2; 218/2; 242/3; 271/3; 33

C:Superfamily: DPRI protein

C:Keywords: transferase

Query Match 56.1%; Score 1353.5; DB 2; Length 470;

Best Local Similarity 57.3%; Pred. No. 1.1e-107; Mismatches 101; Indels 23; Gaps 3;

Matches 255; Conservative 67; Mismatches 101; Indels 23; Gaps 3;

Oy 25 RLVTVOEOMKVEARVGDYRSLFGAAPTSTKIMLEMRDQHEIYLPGLRHMPAFHVL 84

Db 5 KVTTLDEQWYVERREIYDFYSISNPSDLIEIRDKHFGYLSQGLKLPSSVL 64

Oy 85 DANRPWLCYMWVHPLALDLDDLENDIIDFLARCDKDGYSGGPGLPHLATTYAA 144

Db 65 DASRPWLCYMTLHSHIALGESIGKLEDAIDFLTRCDKDGYSGGPGLPHLATTYAA 124

Oy 145 VNTLVTTGSEFALSSINRNLNFMLOMKDVSAPRMHDEIDVRSYTAISVASLVNI 204

Db 125 VNSLTITGKPALSSINRNLNFMLOMKDVSAPRMHDEIDVRSYTAISVASLVNI 184

Oy 205 LDFKLVAGVDYIARCOYTEGGIAGEPYAEAHGCTYFCGLAALLILEAEKVDLPGLIGW 264

Db 185 VDDELHGVGYNYILSCQYEGGIEGSEAHGCTYFCGLAALLILEAEKVDLPGLIGW 244

Oy 265 VAFHOGVECGGRTNKLVDGCTYFMOGAATAFTOKLITIVDKOLKSSYSGKPSGEDAC 324

Db 245 VVFGQVEGEGFGRNTKLVDGCTYFMOGAATAFTOKLITIVDKOLKSSYSGKPSGEDAC 304

Oy 325 ST-----SSY-----GCTAKSSAVDVAKPFDFLOQSNQICPLPHN 362

Db 305 ESELSDDEEHLLEGSSHVQDFPLGQACACENASHSKIAIDVETETINRIAMRPLFDS 364

Oy 363 IALQOYVLLCSQIEVCGRDKPGKGRDYHHCYCLSGLSIAQYSWTDEADSTPLPRDVF 422

Db 365 MYLQOYVLLCSQIEVCGRDKPGKGRDYHHCYCLSGLSIAQYSWTDEADSTPLPRDVF 424

Oy 423 PYSN-LLEPIHPLNVLDKHTAYEF 448

Db 425 PYSKCLLEQVHPLFNVLDRYEAAREY 451

## RESULT 3

J02254

farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta chain - garden pea

N:Alternate names: protein farnesyltransferase beta chain

C:Species: Pisum sativum (garden pea)

C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 26-Aug-1999

C:Accession: J02254

R:Yang, Z.; Cramer, C.L.; Watson, J.C.

Plant Physiol. 101, 667-674, 1993

A:Title: Protein farnesyltransferase in plants. Molecular cloning and expression of a

A:Reference number: J02254; MUID:94105305

A:Accession: J02254

A:Molecule type: mRNA

A:Residues: 1-419 <YAN>

A:Cross-references: GB:L08864

A:Experimental source: apical bud

A>Note: the nucleotide sequence of this paper does not correspond to the sequence of

C:Superfamily: DPRI protein

C:Keywords: heterodimer; transferase

Query Match 54.6%; Score 1315.5; DB 2; Length 419;

Best Local Similarity 56.6%; Pred. No. 1.6e-104;

Matches 252; Conservative 61; Mismatches 93; Indels 39; Gaps 4;

Oy 17 AADPDLRLTVTVQVDEOMKVEARVGDYRSLFGAAPTSTKIMLEMRDQHEIYLPGLRH 76

Db 3 AASTAETPPTVTSQORDQVIESQVFHITQIFANIPMAOSII----- 44

Oy 77 MGPAFHVLDANRPWLCYMWVHPLALDLDDLENDIIDFLARCDKDGYSGGPGLP 136

Db 45 -----RPMWLCYMTLHSHIALGESIGKLEDAIDFLTRCDKDGYSGGPGLP 93

Oy 137 HLAITYAAVMTLVTTGSEFALSSINRNLNFMLOMKDVSAPRMHDEIDVRSYTAISVASLVNI 196

Db 94 HLAITYAAVMTLVTTGSEFALSSINRNLNFMLOMKDVSAPRMHDEIDVRSYTAISVASLVNI 153

Oy 197 SVASVNLIDFLKAKGYDIARCOYTEGGIAGEPYAEAHGCTYFCGLAALLILEAEKVDLPGLIGW 256

Db 154 SVASVNLIDFLKAKGYDIARCOYTEGGIAGEPYAEAHGCTYFCGLAALLILEAEKVDLPGLIGW 213

Oy 257 DLPFLICVAFRQVCEGCGRTNKLVDGCTYFMOGAATAFTOKLITIVDKOLKSSYSGKPSGEDAC 316

Db 214 DLPFLICVAFRQVCEGCGRTNKLVDGCTYFMOGAATAFTOKLITIVDKOLKSSYSGKPSGEDAC 273

Oy 317 RPSG---EDAC---STSSYGCT---AKKSSAVDVAKPFDFLOQSNQICPLPHN 366

Db 274 TVSDAPREKCLDQTSASHATSHIRHEGMNESCSDVKNIGNFISEWROSEPLFHSIALQ 333

Oy 367 QYLLCSQVLEGGIAGEPYAEAHGCTYFCGLAALLILEAEKVDLPGLIGW 426

Db 334 QYLLCSQVLEGGIAGEPYAEAHGCTYFCGLAALLILEAEKVDLPGLIGW 393

Oy 427 LLEPIHPLNVLDKHTAYEF 451

Db 394 LLEPIHPLNVLDKHTAYEF 418

## RESULT 4

A40037

protein farnesyltransferase (EC 2.5.1.-) beta chain - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Oct-1992 #sequence\_revision 16-Oct-1992 #text\_change 05-Nov-1999

C:Accession: A40037

R:Chen, W.J.; Andres, D.A.; Goldstein, J.L.; Russell, D.W.; Brown, M.S.

Cell 66, 327-334, 1991

A:Title: cDNA cloning and expression of the peptide-binding beta subunit of rat p21(r

A:Reference number: A40037; MUID:91309145

A:Accession: A40037

A:Molecule type: mRNA

A:Residues: 1-437 <CHE>

A:Cross-references: GB:M69056; NID:q204185; PIDN:AAA1176.1; PID:q204186

C:Comment: This protein attaches farnesyl residues to a cysteine near the carboxyl te

C:Superfamily: DPRI protein

C:Keywords: heterodimer; transferase

Query Match 39.1%; Score 942.5; DB 2; Length 437;

Best Local Similarity 43.1%; Pred. No. 1.4e-72;

Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;

Oy 5 POSTPTGDDPAAADPDLPR-----LTVTVOEOMKVEARVGDYRSLFGAAPTSTK 56

```

Db 12 PPSSPVWSEPLYSLRPHARERLDDSEVETYSLEQAKVEKEIOEVRSSY---KENLTV 68
Oy 57 IMLEIMRDQHIEYLTPLGRHMGPAFHVLDANKRPMWLCYMMVPHLALDEALDDLENDIID 116
Db 69 PRLVJOREKHNFHYLTKRGRLQRLTDAECCIDASRPWCYWLHSLTELDDEPIPOIVATVDCQ 128
Oy 117 FLARQODDGGYSGSGPGLPHLATYTAAVNTLVYTGSRALSSITRKULYNFMLOMKRVS 176
Db 129 FLELCQSPDGGFGGGPOYPHLAPYAAVMAJCIIGTEEAANVIRELLDYLYLSLKPD 188
Oy 177 GAFRMDGGEIDVRASYAIVASLVNLTDFELKAGVDYIARCOQYRGTAJGEYPAEAH 236
Db 189 GSFLEHWGGEVDVNSATYCAASVASTNLTITPDLEBGTAEWIAFCQNMWEGJGGVPGMAH 248
Oy 237 GGYTFCGALAILLLEAKVDFPLSIGWAFRQ--GVECGFOGRTTKLVDGCGSFWQAGAI 295
Db 249 GGYTTCGIALALVYLKREKSLNKLKSLQWYTSKOMFEBGGFOGRCKMLVDGCTSFQAC-- 306
Oy 296 AFTOKLITIVBKQLSSYCKRPSGEDACSTSSYGCTAKKSSAAYDAKFGFDFTQSGNQ 355
Db 307 -----LPLRLRALHA-----QGDPLALSMHW----- 328
Oy 336 IGRLEFNHALQOYILLCQVULEGILDRPKGNRDRHYSHSCYCLSGLAVSQYSAMDYSGCP 415
Db 329 ---MFHQOALOEYILMCQCPAGSLDRPKGRSDEYHTCYCISGLSIOHFG---SCAM 381
Oy 416 LPOHYLGPYSNLEPIRHPLYNNVLDKHTAYEFSEEE 452
Db 382 LADVVMGVPENVLQPTHRVYVNIQPKVIOATTHFLQK 418

```

RESULT 5  
B49274  
protein farnesyltransferase (EC 2.5.1.-) beta subunit - human  
M:Alternate names: farnesyl-protein transferase beta subunit; FTFase beta subunit; prenyl  
C:Species: Homo sapiens (man)  
C:Date: 25-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-2000  
C:Accession: B49274; I60951  
R:Omer, C.A.; Kral, A.M.; Diehl, R.E.; Prendergast, G.C.; Powers, S.; Allen, C.M.; Gibbs  
Biochemistry 32, 5167-5176, 1993  
A:Title: Characterization of recombinant human farnesyl-protein transferase: cloning, ex  
A:Reference number: A49274; MUID:93264431  
A:Accession: B49274  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-437 <OME>  
A:Experimental source: Placenta  
A>Note: sequence extracted from NCBI backbone (NCBIP:132829)  
R:Andres, D.A.; Milatovich, A.; Ozcelik, T.; Wenzlau, J.M.; Brown, M.S.; Goldstein, J.L  
Genomics 18, 105-112, 1993  
A:Title: cDNA cloning of the two subunits of human CAAX farnesyltransferase and chromos  
A:Reference number: A47659; MUID:94102736  
A:Accession: I60951  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 51-282, 'L', 284-437 <RES>  
A:Molecule type: mRNA  
A:Cross-references: GB:LI0414; NID:g388757; PTDN:AAA86286.1; PID:g388758  
C:Genetics:  
A:Gene: GDB:FNTB  
A:Cross-references: GDB:138174; OMIM:134636  
A:Map position: 14q23-14q24  
C:Superfamily: DpR1 protein  
C:Keywords: transferase

```

Query Match Similarity      39.0%: Score 940.5; DB 2; Length 437:
Best Local Similarity      43.1%: Pred No. 26-72;
Matches 197: Conservative   62; Mismatches 139; Indels 59; Gaps 7

OY      5 POSTPPTGDDPAAPAADPDLPR-----LTVYQVEQMKVEARVGDLYSLGCAAPNTKS 56
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      12 PSSSSVYVSEEPPLYSLRPEARERLDDSVETATYSLEQAVVEEKIDVCFSSY---KNNHLV 68

```

[illegible]

RESULT 6  
 C49274  
 protein farnesyltransferase (EC 2.5.1.-) beta subunit - bovine  
 N:Alternate names: farnesyl-protein transferase beta subunit; FTFase beta subunit; pr  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 25-Feb-1994 #sequenceRevision 18-Nov-1994 #textChange 20-Sep-1999  
 C:Accession: C49274  
 R:Omer, C.A.; Kral, A.M.; Diehl, R.E.; Prendergast, G.C.; Powers, S.; Allen, C.M.; Gi  
 Biochemistry 32, 5167-5176, 1993  
 A:Title: Characterization of recombinant human farnesyl-protein transferase: cloning,  
 A:Reference number: M49274; MUID:93264431  
 A:Accession: C49274  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-437 <OME>  
 A:Experimental source: brain  
 A>Note: sequence extracted from NCBI backbone (NCBIF:132834)  
 C:Superfamily: DPRI protein  
 C:Keywords: transferase

Query Match	39.0%	Score 939.5	DB 2	Length 437
Best Local Similarity	43.1%	Pred No. 2,5e-72		
Matches 197	Conservative 62	Mismatches 139	Indels 59	Gaps 7

  

Qy	5	POSTPTGDDPAAADPLPR-----LVTQVEQMKVEARVDIYSLFGAAPTKS	56
Db	12	PPSSPTINSEPLYSLEPRHARELRDDSEVETYSLEQAVEEKEIOEFSST--KFNHLV	68
Qy	57	IMLELRDQHEIYLPGRHNMGPAPFLVDLANKPMLCYMWHPLALDELALDDLENDIID	116
Db	69	PLVLYQREHNFHYLKRGLQLTDAIYECCLASRPMLCYLHLSLELDEPIPKQVATDVCQ	128
Qy	117	FLARCQDKDGYSGGPGQLPHLATTYAAVNTLVTIGSERALSSINGNLYNPMLOMKDVS	176
Db	129	FLQLCSPREGGSGGGGQGPLHLPATYAAVNAALCIITGEAYIVINREKLYLYLSLKQD	188
Qy	177	GAFRHHDDGEIDVARYSTIISVALINIIIDFLAKVGVGYIARCQVEEGGIGEPALAEH	236
Db	189	GSLFHHDDGEVYVRSATYCAASVALTNITTPDLFEETAIRMQNMEEGIGCVPMEMH	248
Qy	237	GGYTCGGLAALLILNEAEKVDLPSTLIGVAFRQ-GEVCGFQGRFNKLVDCGYSFMQAAI	295
Db	249	GGYTCGGLAALVILNKKERLNLKSLQWYTSQMRREGGFGQGNLVLGSCYSFMQAG--	306

QY 296 AFTOKLITVYDOKSSYSCKRPSGEDACSTSSYGCCTAKKSSSAVDYAKFGFDFIQSSNQ 355  
 Db 307 -----LPI:LLRHLA-----OGDPLSMKRW----- 328  
 QY 356 IGPLFHNIALOOYILLCSQVLEGLRDKPGKRNDRHNSCYCLSGLAIVSYSAMDTGSCP 415  
 Db 329 ---MFHQAOLQBYLTCGCCQCTGGLDKPGKSRPFYHTCYCLSLGSLIAQHFG---SGAM 381  
 QY 416 LPOHVLGPPSYNLEPIHPLVNVLDKRYHTAYEFSEE 452  
 Db 382 LHDVVLGCPENALQPTHPYVNIIGPDKVIQATMHLQK 418

## RESULT 7

T21291  
 hypothetical protein F23B12.6 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T21291  
 R:Wild, A.  
 submitted to the EMBL Data Library, July 1996  
 A:Reference number: 219402  
 A:Accession: T21291  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-401 <WTL>  
 A:Cross-references: EMBL:Z77659; PIDN:CAH01167.1; GSPDB:GN00023; CESP:F23B12.6  
 A:Experimental source: clone F23B12  
 C:Genetics:  
 A:Gene: CESP:F23B12.6  
 A:Map position: 5  
 A:Introns: 29/3; 82/3; 186/3; 252/2; 342/1  
 C:Superfamily: DPr1 protein

Query Match 33.4%; Score 805.5; DB 2: Length 401;  
 Best Local Similarity 38.9%; Pred. No. 6,3e-61;  
 Matches 169; Conservative 75; Mismatches 135; Indels 57; Gaps 6;

QY 22 DLPLVTYQVDMKVEARVGDYRSI---FGAAPTMSIMLELRDQHELYLPGLRHM 77  
 Db 18 DDDNFYTSSTEOKRIETMLEFENSYLVEPFKTSDEDLAEITFRQKHSYLLRLKNC 77  
 QY 78 GPARHVDANRPMLCYMMVHPLALLDEALDDLENDIIDFLARODKDGSGSGPGLPH 137  
 Db 78 PSTATIDASHSMCYGVNALKILDALIPVDYENITIVFLKSCENPEGGSGPGLAH 137  
 QY 138 LATTYAAVNTLVITIGSERLSSINRGNLYNFMLOMKDVSCAFRMHDSGEIDVRASYAIS 197  
 Db 138 LAPTAAVNVCLVSLQKEALRSINRYTLFNPFLKCKHESGFGYHNEGSEIDMSATYALA 197  
 QY 198 VASLVNILDRLAKGVGDYIARCTYEGGIAGEFYEAHGGYTFGGLAALLILNEAKVD 257  
 Db 198 TCEIVGIPMDEISNGVAEWIISCSFEGGFGGEYTEAHGGYTFGCAVASLVLLNRFRLAD 257  
 QY 258 LPSLIGWAFRQ-GVECGFGRTKRLVDGCSFMOGAALAFQTKLITIVYKOKSSYSC 316  
 Db 258 MEGLLRATRRQMRFEQFGRTKRLVDGCSFMOGA-----IFPLDGEHRE---- 306  
 QY 317 RPSGEDACSTSSYGCCTAKKSSSAVDYAKFGFDFIQSSNQIGPLFHNIALOOYILLCSQV 376  
 Db 307 -----GRSLEKG-----LFEAMLEBYILVGCQSV 331  
 QY 377 EGGLRDKPGKRNDRHNSCYCLSGLAIVSYSAMDTGSCPLPQHVHLPYINLEPIHPLYN 436  
 Db 332 HGGGRKDPDPVLDYHNCYVLSGLSVQAKYSLARDK-----ILGDDVMMLAEINPEVN 385  
 QY 437 VVLDKRYHTAYEFPF 450  
 Db 386 VTIASQPAKEFFT 399

## RESULT 8

T37836

probable protein farnesyltransferase (EC 2.5.1.-) beta chain - fission yeast (*Schizosaccharomyces*)  
 C:Species: *Schizosaccharomyces pombe*  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
 C:Accession: T37836  
 R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: 221749  
 A:Accession: T37836  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-382 <MUR>  
 A:Cross-references: EMBL:Z99162; PIDN:CAH16215.1; GSPDB:GN00066; SPDB:SPAC1766.04c  
 A:Experimental source: strain 972h; cosmid c1766  
 C:Genetics:  
 A:Gene: SPDB:SPAC1766.04c  
 A:Map position: 1  
 C:Superfamily: DPr1 protein  
 C:Keywords: transferase

Query Match 25.9%; Score 623.5; DB 2: Length 382;  
 Best Local Similarity 36.2%; Pred. No. 2,2e-45;  
 Matches 152; Conservative 61; Mismatches 144; Indels 63; Gaps 10;

QY 23 LPLVTYQVDMKVEARVGDYRSISLFGAPNTYSIMLELRDQHELYLPGLRHMGRPH 82  
 Db 1 MDELSETOVMQNETATPAVLPPLNG-----ESQSFNIQ-----KHLXYLTQMIDPLPSPT 50  
 QY 83 VLDAANRPMLCYMMVHPLALLDEALDDLENDIIDFLARODKDGSGSGPGLPHLATTY 142  
 Db 51 VLDAANRPMLCYMMVHPLALLDEALDDLENDIIDFLARODKDGSGSGPGLPHLATTY 109  
 QY 143 AAVNTLVITIGSERLSSINRGNLYNFMLOMKDVSCAFRMHDSGEIDVRASYAISV 202  
 Db 110 ASILSICLDSDTAVYSLIERDRLYDWLFLSKNPDGSPRVNNEGSEPARSYAAVCVSLY 169  
 QY 203 NI-LDFRLAKGVGDYIARCTYEGGIAGEFYEAHGGYTFGGLAALLILNEAKVDPLSL 261  
 Db 170 GISMDPLFEGLTQWLCKCCTYEGGSLGYPYEAHGGYTFGGLAALLILNEAKVDPLSL 229  
 QY 262 IGWAFRQVEG-CFGORTKRLVDGCSFMOGAALAFQTKLITIVYKOKSSYSCRPSC 320  
 Db 230 STWLVQRDPAALXGFSGRSKRLVDGCSFMOGAALAFQTKLITIVYKOKSSYSCRPSC 267  
 QY 321 EDACSTSSYGCCTAKKSSSAVDYAKFGFDFIQSSNQIGPLFHNIALOOYILLCSQVLE 379  
 Db 268 -----ASGYSSASHSK-----LPNLFYNPEKLLGYLLQCCQSTSG 303  
 QY 380 LRDKPGKRNDRHNSCYCLSGLA--VSOYSAMDTGSCPLPQHVHLPYINLEPIHPLYN 437  
 Db 304 LRDKPGKRNDRHNSCYCLSGLA--VSOYSAMDTGSCPLPQHVHLPYINLEPIHPLYN 362

## RESULT 9

BVBYP

probable protein prenyltransferase (EC 2.5.1.-) RML - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: DPr1 protein; protein D2412; protein YDL090C

C:Species: *Saccharomyces cerevisiae*  
 C:Date: 31-Mar-1991 #sequence\_revision 23-Aug-1996 #text\_change 16-Jun-2000  
 C:Accession: S67626; S67632; S67633; S67634; S67635; S67636; S67637; S67638; S67639; S67640; S67641; S67642; S67643; S67644; S67645; S67646; S67647; S67648; S67649; S67650; S67651; S67652; S67653; S67654; S67655; S67656; S67657; S67658; S67659; S67660; S67661; S67662; S67663; S67664; S67665; S67666; S67667; S67668; S67669; S67670; S67671; S67672; S67673; S67674; S67675; S67676; S67677; S67678; S67679; S67680; S67681; S67682; S67683; S67684; S67685; S67686; S67687; S67688; S67689; S67690; S67691; S67692; S67693; S67694; S67695; S67696; S67697; S67698; S67699; S67700; S67701; S67702; S67703; S67704; S67705; S67706; S67707; S67708; S67709; S67710; S67711; S67712; S67713; S67714; S67715; S67716; S67717; S67718; S67719; S67720; S67721; S67722; S67723; S67724; S67725; S67726; S67727; S67728; S67729; S67730; S67731; S67732; S67733; S67734; S67735; S67736; S67737; S67738; S67739; S67740; S67741; S67742; S67743; S67744; S67745; S67746; S67747; S67748; S67749; S67750; S67751; S67752; S67753; S67754; 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A:Accession: T37741  
A:Status: preliminary; translated from GB/EMBL/DDAR  
A:Molecule type: DNA  
A:Residues: 1-311 <R1E>  
A:Cross-references: EMBL:AL035248; PIDN:CAA22847.1; GSPDB:GN00066; SPDB:SPAC167.02  
A:Experimental source: strain 972n-; cosmid c167  
C:Genetics:  
A:Gene: SPAC167.02  
A:Map position: 1  
A:Introns: 18/3; 69/1; 108/1; 180/1; 224/3  
C:Superfamily: DPR1 protein

Query Match 13.6%; Score 327.5; DB 2; Length 311;  
Best Local Similarity 24.6%; Pred. No. 3.4e-20;  
Matches 96; Conservative 61; Mismatches 139; Indels 95; Gaps 9;

Qy 58 MLEMRDQHIEYLPGLRHMGPAFHVLDANRPWL-----CYWVHPLALDEALDD 109  
Db 1 MAVLLRRKHISY-----LHDIGNRDELDLFWLKEHLHVSATYWSGMSFWLKKKDDID 53  
Qy 110 LENDIIDFLARCDKDGSGGPGQLPHLATTTAAVNTLVTTIGSERALSSINRGLNFM 169  
Db 54 KER-IVSFLLSCLTESGFGACYPGHDHITNTVYAQVLAWLDS--LHVVDKDKVASIY 109  
Qy 170 LQMDVGAFRPHDGCGLDVAASVAVSLVNIIDPKLAKGVGDYIARQOTEGGIAG 229  
Db 110 IGLQNEGSMKGDWRGWEIDARFVLSGNCIALILGKLDYLNKNTAVDWLMKCYNDGGFGL 169  
Qy 230 EPYEAHNGCYTFCGLAAILLLEAEKVDLPSLIGVAFRGVCEGCGRTKLVDCYSF 289  
Db 170 CPGESHNGAMFTCVAAALKILNKLDLIDELGHWISERQVKGGLNGRPEKLPDSCYGM 229  
Qy 290 WOGAIAFTOKLITIVDKOLKSSYSCKRPSGEDACSTSSYCCATKSSSAVDYAKFDF 349  
Db 230 WDLSPRLAIIIGL-----DW 243  
Qy 350 IOGSONIGPLFHNIALQOYILCSOVLEGLRDKPKGNRDHYHSCYCLSGLAVSQYSAMT 409  
Db 244 IDRQQLI-----DFLIGTODADSGGFADRKEDATDYHRCFSLGLDQF---- 289  
Qy 410 DTGSCPLPQHVLPYSLNLEPIHPLVNVLD 440  
Db 290 -----PN-----IEPVDRFCPLPLE 304

RESULT 12  
S59834  
probable protein prenilyltransferase (EC 2.5.1.?) BET2 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: geranyl-geranyltransferase beta chain; protein P9705.12; protein YPR1  
C:Species: Saccharomyces cerevisiae  
C>Date: 13-Jun-1996 #sequence\_revision 01-Mar-1996 #text\_change 26-Aug-1999  
C:Accession: S59834; S22843; S15399; B32569; S07612  
R:Pauley, A.  
submitted to the EMBL Data Library, April 1995  
A:Description: The sequence of S. cerevisiae cosmid 9705.  
A:Reference number: S59829  
A:Accession: S59834  
A:Molecule type: DNA  
A:Residues: 1-325 <PAU>  
A:Cross-references: EMBL:U25842; NID:g766312; PIDN:AA68110.1; PID:g766324; MIPS:YPR176C  
R:Peterson-Bjorn, S.; Harrington, T.R.; Friesen, J.D.  
Yeast 6, 345-352, 1990  
A:Title: An essential gene in Saccharomyces cerevisiae shares an upstream regulatory ele  
A:Reference number: S22843; WUID:90371957  
A:Accession: S22843  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-21, 'N', 23-325 <PET1>  
R:Rossi, G.; Jiang, Y.; Newman, A.P.; Ferro-Novick, S.  
Nature 351, 158-161, 1991  
A:Title: Dependence of Ypl1 and Sec4 membrane attachment on Bet2.  
A:Reference number: S15399; WUID:91232583  
A:Accession: S15399

A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-322 <NAT>  
R:Peterson-Bjorn, S.; Soltyk, A.; Beggs, J.D.; Friesen, J.D.  
Mol. Cell. Biol. 9, 3698-3709, 1989  
A:Title: PRP4 (RMA4) from Saccharomyces cerevisiae: its gene product is associated w  
A:Reference number: A93112; WUID:89384596  
A:Accession: B32569  
A:Molecule type: DNA  
A:Residues: 1-21, 'N', 23-187 <PET2>  
A:Cross-references: GB:M26597; NID:g172282; PIDN:AA79331.1; PID:g808847  
C:Genetics:  
A:Gene: SCD:BET2  
A:Cross-references: SCD:S0006380; MIPS:YPR176C  
A:Map position: 16R  
C:Superfamily: DPR1 protein  
C:Keywords: transferase

Query Match 13.5%; Score 326; DB 2; Length 325;  
Best Local Similarity 25.4%; Pred. No. 4.8e-20;  
Matches 102; Conservative 61; Mismatches 118; Indels 120; Gaps 14;

Qy 59 LELMRDQHIEYLPGLRHMGPAFHVLDANRPWL-----CYWVHPLALDEAL 106  
Db 5 LTLKEKHIRYI-----ESLDTKKHNEEYMLTEHLRLNGIYWGTLALCVLDSP- 52  
Qy 107 DDDLENDIIDFLARC-ODKDGSGGPGQLPHLATTTAAVNTLVTT-----IGSER--AL 157  
Db 53 ETFFKEEIVSFVLSQMDCKYGAFAFPFRHAILTLTSLAVQILATYDALDYLKDKRVRL 112  
Qy 158 SSINRGLNFMQMKVSCAFRPHDGCGLDVAASVAVSLVNIIDPKLAKGVGDYI 217  
Db 113 ISFIRGN-----QLEDE--GSFGDRGEVDTRVYVALSLSIGLSEVVDPAVDV 164  
Qy 218 ARCOTYEGGIAGEPEYEAHNGCYTFCGLAAILLLEAEKVDLP--SLIGVAFRGVCEG 274  
Db 165 LKCNFPGGGLCPNMAESHAAOAFTCGALAIANKLDMLDDQLEFEGMWLCLERQLEGG 224  
Qy 275 FQGRNKLVDGCYSFWOGAIAFTOKLITIVDKOLKSSYSCKRPSGEDACSTSSYCCATK 334  
Db 225 LMGPRSKLPVPCYSWMVLSLAIIGRL----- 281  
Qy 335 KSSAVDYAKFPGDFTOOSNOIGPLFHNIALQOYILCSOVLEGLRDKPKGNRDHYHSC 394  
Db 252 ---DWINYEK-----LTFEILKQDEKKGISDRPENEVDVFTV 288  
Qy 395 YCLSGLAVSQYSAMTDTGSCPLPQHVLPYSLNLEPIHPLY 435  
Db 289 FGVAAGLS-----LMGTDNLV-PIDPIY 309

RESULT 13  
A53044  
geranylgeranyl-diphosphate geranyltransferase (EC 2.5.1.32) I beta chain - hum  
C:Species: Homo sapiens (man)  
C>Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 24-Nov-1999  
C:Accession: A53044  
R:Zhang, F.L.; Diehl, R.E.; Kohl, N.E.; Glibos, J.B.; Giros, B.; Casey, P.J.; Omer, C.  
J. Biol. Chem. 269, 3175-3180, 1994  
A:Title: CDNA cloning and expression of rat and human protein geranylgeranyltransfera  
A:Reference number: A53044; WUID:94148804  
A:Accession: A53044  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-377 <ZHA>  
A:Cross-references: GB:L25441; NID:g466490; PIDN:AAA35888.1; PID:g466491  
C:Genetics:  
A:Gene: GDB:PGRT1B; GGT1; BGG1  
A:Cross-references: GDB:305477  
C:Superfamily: cell division control protein CDC43  
C:Keywords: transferase

Query Match 13.3%; Score 320; DB 2; Length 377;





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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2002, 17:08:30 ; Search time 20 Seconds  
(without alignments)

875.062 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411  
Sequence: 1 MDPSQSTPTGDDPAAAD.....PLYNVLDKRYHAYEFSSE 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315.5	54.6	419	1 PPTB_PEA	004903 pisum sativ
2	1155.5	47.9	404	1 PPTB_ARATH	038970 arabidopsis
3	944.5	39.2	437	1 PPTB_BOVIN	P49355 bos taurus
4	942.5	39.1	437	1 PPTB_RAT	002293 rattus norv
5	940.5	39.0	437	1 PPTB_HUMAN	P49356 homo sapien
6	618.5	25.7	431	1 RAM1_YEAST	P22057 saccharomyc
7	343.5	14.2	341	1 BERT_CANAL	093830 candida alb
8	327.5	13.6	311	1 PPTB_SCHPO	P46960 schizosacch
9	326	13.5	325	1 BERT_YEAST	P20133 saccharomyc
10	320	13.3	377	1 PGT1_HUMAN	P53609 homo sapien
11	313	13.0	377	1 PGT1_RAT	P53610 rattus norv
12	297.5	12.3	355	1 PPTB_CAEEL	P41992 caenorhabdi
13	289.5	12.0	325	1 CMG2_SCHPO	P32434 schizosacch
14	282	11.7	331	1 PGTB_HUMAN	008603 rattus norv
15	280	11.6	331	1 PGTB_HUMAN	P53611 homo sapien
16	278	11.5	339	1 PGTB_MOUSE	P53612 mus musculu
17	190.5	7.9	376	1 CAL1_YEAST	P07207 saccharomyc
18	97	4.0	1090	1 PULA_KLEPN	P18898 klebsiella
19	96.5	4.0	2703	1 NOTC_DROME	P07207 drosophila
20	95.5	4.0	705	1 CMBA_BACSU	002113 bacillus su
21	90	3.7	343	1 RECR_BPP1	P06956 bacteriopho
22	89.5	3.7	334	1 CATL_BOVIN	P25975 bos taurus
23	89.5	3.7	334	1 CATL_PIG	Q28944 sus scrofa
24	89.5	3.7	704	1 DP3E_RHOCA	008045 rhodobacter
25	89	3.7	679	1 TKT1_KLULA	Q12630 kluyveromyc
26	88	3.6	734	1 PUR1_ZYMO	094966 zymomonas m
27	87	3.6	334	1 CATL_RAT	P07154 rattus norv
28	86.5	3.6	515	1 TRPE_BACSU	P03963 bacillus su
29	86.5	3.6	779	1 SNL1_MOUSE	Q06070 mus musculu
30	86	3.6	368	1 PEPO_LACHE	084913 lactobacill
31	86	3.6	522	1 Y4LR_RHISN	P55558 rhizobium s
32	86	3.6	759	1 CAS1_ARATH	P38605 arabidopsis
33	86	3.6	1298	1 ICP4_HSV11	P08392 herpes simp

34	85.5	3.5	998	1 LONH_PYRAB	Q09c6 pyrococcus
35	85	3.5	1066	1 ITA3_HUMAN	P26006 homo sapien
36	84.5	3.5	521	1 NIFK_AZOB	P25314 azospirillum
37	84.5	3.5	702	1 LONH_HALNL	09sc3 halobacteri
38	84.5	3.5	2832	1 NDVH_RHIME	P20471 rhizobium m
39	84	3.5	334	1 CATL_MOUSE	P06797 mus musculu
40	84	3.5	684	1 FBIL_CHICK	073775 gallus gall
41	84	3.5	5376	1 ZAN_MOUSE	088799 mus musculu
42	83.5	3.5	986	1 GUN2_CLOSR	P23659 clostridium
43	83	3.4	265	1 UBIE_RICPR	09zcp3 rickettsia
44	83	3.4	668	1 PAB5_ARATH	005196 arabidopsis
45	82.5	3.4	880	1 GUN4_THIEFU	P26221 thermomonos

## ALIGNMENTS

RESULT 1  
PPTB\_PEA STANDARD; PRT; 419 AA.  
AC Q04903;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Protein farnesyltransferase beta subunit (EC 2.5.1.-) (CAAX  
DE farnesyltransferase beta subunit) (RAS proteins prenyltransferase  
DE beta) (Fase-beta).  
GN PPTB.  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SRRAIN-CV, ALASKA, TISSUE-Seeding;  
RX MEDLINE=94105305; Pubmed=8278509;  
RA Yang Z., Cramer C.L., Watson J.C.;  
RT "Protein farnesyltransferase in plants. Molecular cloning and  
RT expression of a homology of the beta subunit from the garden pea.";  
RL Plant Physiol. 101:667-674(1993).  
CC -!- FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM  
CC FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM  
CC THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS  
CC RESPONSIBLE FOR PEPTIDE-BINDING (BY SIMILARITY).  
CC -!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).  
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT  
CC FAMILY.  
CC -!- SIMILARITY: CONTAINS 5 PPTB REPEATS.  
CC -----  
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CC -----  
CC EMBL: L08664; AAA3649.1; -.  
CC PIR: JQ2254; JQ2254.  
CC DR HSSP: Q02293; 1FT1.  
CC DR InterPro: IPR001330; Prenyltrans.  
CC DR Pfam: PF00432; Prenyltrans; 5.  
CC KW Transferase; Prenyltransferase; Repeat; zinc.  
CC FT REPEAT 68 109 PPTB 1.  
CC FT REPEAT 119 160 PPTB 2.  
CC FT REPEAT 167 208 PPTB 3.  
CC FT REPEAT 215 256 PPTB 4.  
CC FT REPEAT 329 371 PPTB 5.  
CC FT METAL 241 241 ZINC (BY SIMILARITY).  
CC FT METAL 243 243 ZINC (BY SIMILARITY).



```

Db      301 T-----YINRMQL-VFDSLGLQRYVLLCSK IPDGGRDKPKPRDFHRTCYCL 348
Oy      398 SGLANSQSAMTDGSCPLPOHVIGPYNLLEPHILNVNVDKHHTAYEEF 449
       |||:::~::~~::~|||:::~::~~::~|||:::~::~~::~|||:::~::~~::~|||
Dd      349 SGLVAQAHAWLKDDEPTPLTRDIMKGYSNLPLEVOLLIHNIVMDQYNEAIEFF 400

RESULT 3
PF7B_BOVIN STANDARD PRT; 437 AA.
AC p49355.Q8T5Z5;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein farnesyltransferase beta subunit [EC 2.5.1.-] (CAAX
   farnesyltransferase beta subunit) (RAS proteins prenyltransferase
   beta).
FM Bos taurus (Bovine).
GC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Bovinae; Bos.
RN NCBI_TaxID=9913;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93264431; PubMed=8494894;
RA Omer C.A., Kral A.M., Dielh R.E.; Prendergast G.C., Powers S.,
RA Allen C.M., Gibbs J.B., Kohl N.E.;
RT "Characterization of recombinant human farnesyl-protein transferase:
RT cloning, expression, farnesyl diposphate binding, and functional
RL homology with yeast prenyl-protein transferases."
RL Biochemistry 32:5167-5176(1993).
CC -I FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
CC FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
CC THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
CC RESPONSIBLE FOR PEPTIDE-BINDING.
CC -I COPACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -I SUBUNT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -I SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSEFERASE BETA SUBUNIT
CC FAMILY.
CC -I SIMILARITY: CONTAINS 5 PF7B REPEATS.
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DR EMBL; L00633; AAA30524.1; -.
DR HSSP; Q02293; lpf2.
DR InterPro; IPR001330; Prenyltrans.
DR Pfam; PF00432; Prenyltrans; 5.
KW Transferase; Prenyltransferase; Repeat; Zinc.
FT FT          123    164            PF7B 1..
FT REPEAT     174    215            PF7B 2..
FT REPEAT     222    263            PF7B 3..
FT REPEAT     270    312            PF7B 4..
FT REPEAT     332    374            PF7B 5..
FT METAL      297    297            ZINC (BY SIMILARITY).
FT METAL      299    299            ZINC (BY SIMILARITY).
FT METAL      362    362            ZINC (BY SIMILARITY).
SO SEQUENCE 437 AA; 48767 MW; CE09DA86ACAB64 CRC64;

Query Match           39.2%; Score 944.5; DB 1: Length 437;
Best Local Similarity 43.3%; Pred. No. 5.6e-74;
Matches 198; Conservative 62; Mismatches 138; Indels 59; Gaps 7;
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Db      12  PSSSSPISEPLSEPLYSIREPHAREERLQDDSVETVSTIEQAKVEEKIOEVESSY----KFNHLV  66
Oy      57  IMLELMNRQHTIEYLTPGCRHNGPRAFHVIDANRPMPLCYWMHPLALDEALDDLENDIID  116
Db      69  PRLVYQREKHHYLRKGLRQLDTDAECLDASRPMPLCYWLHSLLELDEPIQMAWDVCO  128
Oy      117 FLARCODEKDGYSGGPGQLPHLATTYAENVLTLYIGSERALSSINRGNTLYNFMLOMKDVS  176
Db      129 FLELCQSPREGFGGGPGQGYPLHPLATYAENVNLCLIGTEBAVDYINRKKLQYLYLSLKQPD  188
Oy      177 GAFRRHDCGGLIDVRASTAYSAISVNLVILDFKLAKGYGVYIARQYTEGGIAGEPTAEAH  236
Db      189 GSFLLHDDGDEVDSVSAVCMAASVSLTNTLPDLEPGTAEMVIAAROMEGGIGVPGMEAH  248
Oy      237 GGYFGFCGLAAILILNLEAKRVDLPISLIGVAFRQ-GVECGRGFGFRNKLYVDCSPFGQAAI  295
Db      249 GGYTFPGCLAAVLYILKKESLMLKSLLOLVYTSRQMRFBEGFGQGRNKLVDGCTSPMQMG--  306
Oy      296 AFTOKLITIVDKLSSYSYSCRPSGEGDACSTSSYGCYTAKKSSSAVDYAKRFPDFIOOSNQ  355
Db      307 -----LLEPLLRALHA-----OGDPLASMSR-----  328
Oy      356 IGPLRHNIALDOYITLISQVLEGGIRPKPGKNRQHHYSYCYLGLAVSOYSAMTDGSCP  415
Db      329 ---MHQDALDEYILIMCCQCTPTGGLDLPKGSRSRPFYHCTCLSGLSIAQHFQ-----SGAM  361
Oy      416 LPOHVIQPSYSNLPEIHPPLVNVVLDRKYATAEPFSE  452
Db      382 LHDVVLGYVENALQPTHPVYNIIGDPKVIAQATMHFLQK  418

RESULT 4
PFTB_RAT
PFTB_RAT      STANDARD:      PRT:  437 AA.
AC      002293;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Protein farnesyltransferase beta subunit (EC 2.5.1.-) (CAAX
      farnesyltransferase beta subunit) (RAS proteins prenyltransferase
      beta) (Frase-beta).
      FMTB.
GN      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
      (1)
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP      TISSUE-Brain:
RX      ChemW-91309145; PubMed=1855253;
      Medline=91309145.
RT      Chen W.-J., Andres D.A., Goldstein J.L., Russell D.W., Brown M.S.;
      "cDNA cloning and expression of the peptide-binding beta subunit of
      rat p21ras farnesyltransferase, the counterpart of yeast 3Pr4/RAM1";
      RL      Cell 66:337-344(1991).
      (2)
RP      X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
RX      MEDLINE=97218306; PubMed=9065406;
      Medline=97218306.
RT      Park H.-W., Boduluri S.R., Moosaw J.F., Casey P.J., Beese L.S.;
      "Crystal structure of protein farnesyltransferase at 2.25-A
      resolution.";
      RL      Science 275:1800-1804(1997).
      (3)
RP      X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RX      MEDLINE=98322062; PubMed=9657673;
      Medline=98322062.
RT      Long S.B., Casey P.J., Beese L.S.;
      "Co-crystal structure of protein farnesyltransferase complexed with a
      farnesyl diphosphate substrate.";
      RL      Biochemistry 37:9612-9618(1998).
CC      -1- FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
      FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
      THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
      RESPONSIBLE FOR PEPTIDE-BINDING.
      -1- COFACTOR: BINDS ONE ZINC ION.

```

```

CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 5 PFTB REPEATS.
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CC -----
CC EMBL: M69056; AAA41176.1; -.
CC PIR: A40037; A40037.
CC PDB: 1FT1; 18-NOV-98.
CC PDB: 1FT2; 18-NOV-98.
CC InterPro: IPR001330; Prenyltrans.
CC Pfam: PF00432; Prenyltrans.
CC Transferase; Prenyltransferase; Repeat; Zinc; 3D-structure.
CC REPEAT 123 164 PFTB 1.
CC REPEAT 174 215 PFTB 2.
CC REPEAT 222 263 PFTB 3.
CC REPEAT 270 312 PFTB 4.
CC REPEAT 332 374 PFTB 5.
CC METAL 297 297 ZINC.
CC METAL 299 299 ZINC.
CC METAL 362 362 ZINC.
CC SEQUENCE 437 AA; 48673 MW; 41A9D6D79CD319A8 CRC64;

Query Match 39.18; Score 940.5; DB 1; Length 437;
Best Local Similarity 43.18; Pred. No. 8.3e-74;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAADADLPR-----LTVQVEQMKYARVGDYRSIFGAAPNTKS 56
D 12 PSSSPVWSEPLYSRPHARELRDDSDSEVTIVSIEQAKVEKIQEYVSSY---KFNHLV 68
QY 57 IMLEMRQHIETPLGLRHMGPAFHVLDANRPMVLCYVMVPLALDLBALDDLENDIID 116
D 69 PRLVQREKHRYLKRGLQRLTDAYECIDASRPMVLCYWLHSLDLDEPIQIVATDVQC 128
QY 117 FLARQDQDGGYSGGPGQLPLATTYAAVNTLVITGSEFALSSINRGLYNFMLOMKVYS 176
D 129 FLELCQSDGDFGGPGQYPIHAPTYAVNALCTIGTEAVYNVIREKLYLVSLKOPD 188
QY 177 GAFRMHDCGLDVASATYATISVASLVNTLDFKLAKGVADYIARCOYEGGIAGEPYAEAH 236
D 189 GSFIMHVGCEYDVASVACASVASLTNITTPDLEGTAEVIMARQNMGGIGVPMGEAH 248
QY 237 GGYTFCCGIALILNEAEKVLPSLIGVAFRQ-GVECGFGQRTNKLYDGCYSFMOCAAI 295
D 249 GGYTFCCGIALILNEAEKVLPSLIGVAFRQ-GVECGFGQRTNKLYDGCYSFMOCAAI 306
QY 296 AFTOKLITIVKOLKSSYSCKRPSGDEDCSTSSYGCTAKKSSAVADAKFGFDIQOSNQ 355
D 307 -----LPLRLRALHA-----GQDPALSMH----- 328
QY 356 IGLPFIHNTALQOYITLLSQVLEGLRDKPGKNRDHYHSCYCLSGLAVSQYSAMTDGSCP 415
D 329 ---MFHOALQEXILMCCQCPAGGLDKPKSRDFFHYHCYCLSGLSIAQHG---SGAM 381
QY 416 LPOHVLGPRYSMLERPHILYLVNVDLKYHTAEFFSEE 452
D 382 LHDVVMGVENVLQPTHPVYVIGPDKVIOATTHFLQK 418

RESULT 5
PFTB_HUMAN STANDARD; PRT; 437 AA.
AC P49356;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein farnesyltransferase beta subunit (EC 2.5.1.-) (CAAX
DE farnesyltransferase beta subunit) (RAS proteins prenyltransferase
DE beta) (Frase beta).
CN FNTB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleota; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93264431; PubMed=8494894;
RA Allen C.A., Kral A.M., Diehl R.E., Prendergast G.C., Powers S.,
RT "Characterization of recombinant human farnesyl-protein transferase:
RT cloning, expression, farnesyl diphosphate binding, and functional
RT homology with yeast prenyl-protein transferases."
RL Biochemistry 32:5167-5176(1993).
RN [2]
RP SEQUENCE OF 51-437 FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94102736; PubMed=8276393;
RA Andres D.A., Milatovich A., Ozcelik T., Wenzlau J.M., Brown M.S.,
RT Goldstein J.L., Francke U.;
RT "CDNA cloning of the two subunits of human CAAX farnesyltransferase
RT and chromosomal mapping of FNTA and FNTB loci and related
RT sequences."
RL Genomics 18:105-112(1993).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
CC FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
CC THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
CC RESPONSIBLE FOR PEPTIDE-BINDING.
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -----
CC -1- SIMILARITY: CONTAINS 5 PFTB REPEATS.
CC -----
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CC -----
CC EMBL: L00635; AAA3854.1; -.
CC EMBL: L10414; AAA86286.1; -.
CC HSP: 002293; 1FT2.
CC MIM: 134636; -.
CC InterPro: IPR001330; Prenyltrans.
CC Pfam: PF00432; Prenyltrans.
CC Transferase; Prenyltransferase; Repeat; Zinc.
CC REPEAT 123 164 PFTB 1.
CC REPEAT 174 215 PFTB 2.
CC REPEAT 222 263 PFTB 3.
CC REPEAT 270 312 PFTB 4.
CC REPEAT 332 374 PFTB 5.
CC METAL 297 297 ZINC (BY SIMILARITY).
CC METAL 299 299 ZINC (BY SIMILARITY).
CC METAL 362 362 ZINC (BY SIMILARITY).
CC CONFLICT 283 283 R -> L (IN REF. 2).
CC SEQUENCE 437 AA; 48773 MW; 8E8E571846146709 CRC64;

Query Match 39.08; Score 940.5; DB 1; Length 437;
Best Local Similarity 43.18; Pred. No. 1.2e-73;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAADADLPR-----LTVQVEQMKYARVGDYRSIFGAAPNTKS 56
D 12 PSSSPVWSEPLYSRPHARELRDDSDSEVTIVSIEQAKVEKIQEYVSSY---KFNHLV 68

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DE Type II proteins geranyltransferase beta subunit (EC 2.5.1.-)
DE (type II protein geranyltransferase beta subunit) (GCase-II-
DE beta) (PGT) (PPT1/SEC4 proteins geranyltransferase beta
DE subunit).
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
ON NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10231;
RA Ishii N., Aoki Y., Aisawa M.;
RT Molecular cloning of BET2 gene from Candida albicans.
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
CC GERANYLERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL
CC X-CC OR X-C-X-C, WHERE BOTH CYSTEINES MAY BECOME MODIFIED. ACTS
CC ON YPT1 AND SEC4 (BY SIMILARITY).
CC -1- COPFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 6 PPTB REPEATS.
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CC -----
DR EMBL: AB021171; BAA5193.1; -
DR HSSP: Q02293; 1FT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 5.
KW Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 15 55 PPTB 1.
FT REPEAT 62 104 PPTB 2.
FT REPEAT 122 163 PPTB 3.
FT REPEAT 170 211 PPTB 4.
FT REPEAT 223 264 PPTB 5.
FT REPEAT 271 313 PPTB 6.
FT METAL 249 249 ZINC (BY SIMILARITY).
FT METAL 251 251 ZINC (BY SIMILARITY).
FT METAL 301 301 ZINC (BY SIMILARITY).
SO SEQUENCE 341 AA; 38460 MW; 24A89E11F911488 CRC64;

Query Match 14.2%; Score 343.5; DB 1; Length 341;
Best Local Similarity 25.0%; Pred. No. 3.3e-22;
Matches 92; Conservative 65; Mismatches 138; Indels 73; Gaps 8;

DB 52 PNRKSIWLELMRHOIHLYLPGRLHMKRPAHVIVDANRPMVLGMVYHPLALLDEALDDLE 111
DB 6 PDEKVIILFD--KSKHVQYIVEDSHRSFEWLESHLRMCLYMGVATLLITMNE-LSALAQ 62
DB 112 NDIIDFLARC-QDKDGYSGPGOLPHLATTYAAVNTLVITGSPRALSTIN-----R 162
DB 63 QDVIDYIMLCMDKDKTGFAGSFPKHGDIITLSLALQYLKTIYDEQLVLYLNNNESSGNKR 122
DB 163 GNLVNFMLQMKDVSGAFRMHGDGEIDVRSYTAISVASLVNITLDFKLAKGVGYIARQQT 222
DB 123 ERLIKFTIGQLPDSGFGDKYGEVDFRFTYVAVSSLSLNLALDTSIAADTASAFIMQCFN 102
DB 223 YEGGIAEPYAEAHGCTPGCLALLILNDEAKYDPS---LIGVAFRQGVCC-GEFG 277
DB 183 FDGCGFLIPGSESHAAQVFTCVGALIMNKLIDLVDENKRVKLLDWLTEROVLPSGGFNG 242
DB 278 RTMKLVDCGCSFPMGAAIAFTQKLIITVDQKLSSYSCKRPSGDACSTJSTCYCTAKKSS 337
DB 243 RPEKLPVCTYSMWVLSLSLIL-----KRR 266

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QY 338 SAVDYAFGDFEIQOSNQIGPLFNHIALQOYILCSQVLEGLRDKPGKRDHYHSCYCL 397
DB 267 NMDVLDK-----ILENFILTCQDLENGFSDRNGTQDYVHHCFAI 306
QY 398 SGLAVSOY 405
DB 307 AGLSLDY 314

RESULT 8
PPTB_SCHPO STANDARD; PRT; 311 AA.
ID PPTB_SCHPO
AC P46960;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type II proteins geranyltransferase beta subunit (EC 2.5.1.-)
DE (type II protein geranyltransferase beta subunit) (GCase-II-
DE beta).
DE PBT1 OR SPAC167.02.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
ON NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96310627; PubMed=8740421;
RA Godfrey R., Davey J.;
RT "Sequence of PBT1, a gene for the beta subunit of the type-II
RT geranyltransferase from the fission yeast Schizosaccharomyces
RT pombe."
RL Yeast 12:479-482(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=9721.
RA Rieger M., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
CC GERANYLERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL
CC X-CC OR X-C-X-C, WHERE BOTH CYSTEINES MAY BECOME MODIFIED.
CC -1- COPFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 5 PPTB REPEATS.
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CC -----
DR EMBL: X92183; CAA63094.1; -
DR EMBL: AL035248; CAA22847.1; -
DR HSSP: Q02293; 1FT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 5.
KW Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 54 95 PPTB 1.
FT REPEAT 102 143 PPTB 2.
FT REPEAT 150 191 PPTB 3.
FT REPEAT 197 239 PPTB 4.
FT REPEAT 246 288 PPTB 5.
FT METAL 224 224 ZINC (BY SIMILARITY).
FT METAL 226 226 ZINC (BY SIMILARITY).
FT METAL 276 276 ZINC (BY SIMILARITY).
SO SEQUENCE 311 AA; 35092 MW; 2AB617C769D3B08 CRC64;

Query Match 13.6%; Score 327.5; DB 1; Length 311;

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Best Local Similarity 24.6%; Pred. No. 7e-21;

Matches 96; Conservative 61; Mismatches 139; Indels 95; Gaps 9;

```

QY 58 MLEMRDQHIEYLTPLGRHMGPAFHVLDANRPYL-----CYMMVHPALIDEALDD 109
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 1 MAVLLRDKHISY-----LHDSGNRTDELDF---WLKEHLHSAITYNCSMWLKKKDDID 53
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 110 LENDIIDFLARCDDKDGYSGGFGQLPHLATTYAAVNTLVTTIGSERALSSINGNLNFEM 169
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 54 KER-IYSFLLSCLTESGCFACYPGHDDHTNTYAVAVLMLDS---LHVVDKDKVASYI 109
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 170 LQMKDVSCAFRMHDGEIDYRASYTAISVALYNIIDFKIAKGVGYIARQYIEGGIAG 229
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 110 IGLQNDGSGSKDGWRGEIDARFLYSGINCLALIGLKDYLNNKRAVYMLKCYNPDGFGFL 169
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 230 EPPAEEAGGYTCFGLAALLILNEAEKVYDPLSLIGVAFFRGVCEGFGFGRNKLVDGYSF 289
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 170 CPQAEHSGANVFCTVAALIKLNLKLDLIDELLGWMISEKRYKGGGLNGREKLPDSCYGM 229
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 290 WOGAIAIAFTOKLITIVDKOLKSSYSCKRPSGEDACSTSSYGTAKKSSSAVDYAKGDF 349
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 230 WDSLPLAIIIGKL-----DW 243
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 350 IOOSNIGPLFHINIALOQYITLCSQVLEGLRPKPKNRDHYHSCYCLSGIAYSQTSAMT 409
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 244 IDRNQIL-----DPLLTGTQADSGGFADRKEDADVDYHTCFSLAGLSILOF--- 289
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 410 DTGSCPLPQHVLGPGYSNLLEPIHLYNVVD 440
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 290 -----PN-----IEPVDPRCLPLE 304
| : : : : : | : : : : | : : : : | : : : : | : : : : |

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RESULT 9  
BET2\_YEAST  
ID BET2\_YEAST STANDARD; PRT; 325 AA.  
AC P20133; P32433;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Type II proteins geranylgeranyltransferase beta subunit (EC 2.5.1.-)  
DE (Type II protein geranylgeranyltransferase beta subunit) (GGTase-II-beta) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase beta subunit).  
DE subunit).  
GN BET2 OR YPR176C OR P9705.12.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90371957; PubMed=2204247;  
RA Petersen-Bjoern S., Harrington T.R., Friesen J.D.;  
RA "An essential gene in Saccharomyces cerevisiae shares an upstream regulatory element with PRP4.";  
RT Yeast 6:345-352(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91232583; PubMed=1903184;  
RA Rossi G., Jiang Y., Newman A.P., Ferro-Novick S.;  
RA "Dependence of Ypt1 and Sec4 membrane attachment on Bet2.";  
RT Nature 351:158-161(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=288C / AB972;  
RA Johnson M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucha T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Marids E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevisan E., Vignati D., Wilcox L., Wohlman P., Vaudin R., Vaudin R., Waterston R.;  
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [4]

```

RP SEQUENCE OF 1-187 FROM N.A.  
RX MEDLINE=89384596; PubMed=2528686;  
RA Peterson-Bjoern S., Soltyk A., Beggs J.D., Friesen J.D.;  
RT "PRP4 (RNA4) from Saccharomyces cerevisiae: its gene product is associated with the u4/u6 small nuclear ribonucleoprotein particle.";  
RL Mol. Cell. Biol. 9:3698-3709(1989).  
RN [5]  
RP CHARACTERIZATION.  
RX MEDLINE=94050127; PubMed=8232542;  
RA Jiang Y., Rossi G., Ferro-Novick S.;  
RT Bet2p and Mad2p are components of a prenyltransferase that adds geranylgeranyl onto Ypt1 and Sec4p.";  
RL Nature 366:84-86(1993).  
CC -I- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL X-CC OR X-C-X-C, WHERE BOTH CYSTEINES MAY BECOME MODIFIED. ACTS ON YPT1 AND SEC4.  
CC -I- CORFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).  
CC -I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.  
CC -I- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT FAMILY.  
CC -I- SIMILARITY: CONTAINS 6 PEST REPEATS.  
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CC -----  
CC EMBL; M29585; AAA66939.1; -  
CC EMBL; M26597; AAA79331.1; -  
CC EMBL; U25842; AAB68110.1; -  
CC PIR; S22843; S22843.  
CC DR; B32569; B32569.  
CC HSSP; Q02293; IFT2.  
CC SGD; S0006380; BET2.  
CC InterPro: IPR001330; Prenyltrans.  
CC DR Pfam: PF00432; Prenyltrans; 5.  
CC K transferase; Prenyltransferase; Repeat; Zinc.  
FT REPEAT 9 50  
FT REPEAT 57 99  
FT REPEAT 109 150  
FT REPEAT 157 198  
FT REPEAT 208 249  
FT REPEAT 256 298  
FT REPEAT 234 234  
FT METAL 236 236  
FT METAL 286 286  
FT METAL 286 286  
FT CONFLICT 22 22  
SQ SEQUENCE 325 AA; 36666 MW; 6A9C4ADFBE2AFAFC CRC64;  


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Query Match 13.5%; Score 326; DB 1; Length 325;  
Best Local Similarity 25.4%; Pred. No. 1e-20;  
Matches 102; Conservative 61; Mismatches 118; Indels 120; Gaps 14;

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QY 59 IELMRDQHIEYLTPLGRHMGPAFHVLDANRP-----WU-----CYMMVHPALIDEAL 106
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 5 IYLLKKEHISY-----ESLDTKKNHFEYMLTERLNGIYWGTCALCVLDSP- 52
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 107 DDDLENDIIDFLARC-QDKRGYSGFGQLPHLATTYAAVNTLVT-----ISER--AL 157
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 53 ETPVKEEIVISFVLSWDDKYGAFAPRRDANLITLSAVQIATYDALDVLKDKRVRL 112
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 158 SSINSGNLVYFMLQMDVSGAFRMHDGEIDYRASYTAISVALYNIIDFKIAKGVGYI 217
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 113 ISFTIRG-----QLED--GSFQDREGEVDTRFYTTALSILDELTSEVVDPAVDY 164
| : : : : : | : : : : | : : : : | : : : : | : : : : |
QY 218 ARCOTYEGGIAGEPYAEAGHYTCFGLAALLILNEAEKV---DPLSLIGVAFRGVECG 274
| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 165 LKCYNDGCGFGLCPNESHAAQAFCTGALAIANKIKMLSDDLLEELGWMICEROLPEGS 224
| : : : : : | : : : : | : : : : | : : : : | : : : : |

```

QY 275 FQGTNNKLVDCYSFQWGAALAFQKLTITVDKQKSSYCKRPSGEDASTSYSGCTAK 334  
 DB 225 LMGPRSLPDCYSWMVSLALIGRL----- 251  
 QY 335 KSSAVVYAKGFCFPIQOSNIGPLFNHIALQOYILLCQVLEGGLKDKPKGNHDHYSK 394  
 DB 252 ----DWINTERK-----LTERILKCODEKKGIGSDRPNENEVDHRTV 288  
 QY 395 YCLSLGLAVSOYSAMTDGSCPLPQHVILGPPYSNLEPIHPLY 435  
 DB 289 FGVAIGLS-----LMGYDNLV-PLDPIY 309

RESULT 10  
 PGTL\_HUMAN STANDARD; PRT; 377 AA.  
 ID PGTL\_HUMAN  
 AC P53609;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Geranylgeranyl transferase type I beta subunit (EC 2.5.1.-) (Type I  
 protein geranyl-geranyltransferase beta subunit) (GGTase-I-beta).  
 GN PGGT1B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta, and Kidney;  
 RX MEDLINE=94148804; PubMed=8106351;  
 RA Zhang F.L., Diehl R.E., Kohl N.E., Gibbs J.B., Giros B.,  
 RA Casey P.J., Omer C.A.;  
 RT "cDNA cloning and expression of rat and human protein  
 geranylgeranyl transferase type-I.";  
 RL J. Biol. Chem. 269:3175-3180(1994).  
 CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM  
 GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL  
 SEQUENCE CYS-ALIPHATIC-ALIPHATIC-X. ACTS ON THE RAC1, RAC2,  
 CC RAP1A AND RAP1B PROTEINS.  
 CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT  
 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 4 PPTB REPEATS.  
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 CC -----  
 CC EMBL: L25441; AAA35888.1; -.  
 DR HSSP: 002293; 1FT1.  
 DR MIM: 602031; -.  
 DR InterPro: IPR001330; Prenyltrans.  
 DR Pfam: PF00432; Prenyltrans; 5.  
 KW Transferase; Prenyltransferase; Repeat; Zinc.  
 FT REPEAT 144 186 PPTB 1.  
 FT REPEAT 193 234 PPTB 2.  
 FT REPEAT 245 284 PPTB 3.  
 FT REPEAT 291 333 PPTB 4.  
 FT METAL 269 269 ZINC (BY SIMILARITY).  
 FT METAL 271 271 ZINC (BY SIMILARITY).  
 FT METAL 321 321 ZINC (BY SIMILARITY).  
 SQ SEQUENCE 377 AA; 42396 MW; 565CD9B6C087AADF CRC64;

Query Match 13.3%; Score 320; DB 1; Length 377;  
 Best Local Similarity 26.5%; Pred. No. 4e-20;  
 Matches 110; Conservative 62; Mismatches 121; Indels 122; Gaps 18;

QY 59 LEIMRDQHIIEYLPGLRHMGPAFVLDANRPMWCVHPLALLDDEALDDLENDIIDF- 117  
 DB 18 LDFLDRHVAHFQRCQLOVLEPERSLSLETSLRTIAFALSCGLMDLD-SLDVVRNDDIIEVI 76  
 QY 118 -----LARCQKDGCGYSG--GGQLP-----HLATTAANVTLVTTG 152  
 DB 77 YSLQVLPTEDRSNLMRCGFGSSYLGIPIFNPSSAPGTAHPYDSGHIAMTYTGISCLVILG 136  
 QY 153 SERALSSINGNLNYNFM--LQMKDVSCAF-RMHGDGIDVRASVTAISVALYNI--LD 206  
 DB 137 DD--LSLVNKEACIAGIALQLED--GSFCVAEGSSNDKRFYVYCACTCYMLNMSGMD 192  
 QY 207 FKLAKGYDYIARCQYEGGIAEPEYEAHGYTFGGLAAILLNEAEKY---DLPSLI 262  
 DB 193 MKKAI--TYIRSMYSYDNLCAQAGLSEHGSGTFGCIALCLMGKLEEVFSEKELMRK 249  
 QY 263 GWAFRGVCEGFGQGRNKLVDGCYSFWGAAALAFQKLTITVDKQKSSYCKRPSGED 322  
 DB 250 RWCIMRG--ONGYHGRNKPVDICYSFWGA---TLKLKTI----- 285  
 QY 323 ACSTSYCYTAKKSSAVDAKFCGDFIQOSNIGPLFNHIALQOYILLCQVLEGGLRD 382  
 DB 286 -----FOYTNF-----EKN-----RNILSTQDRLVGSGFAK 311  
 QY 383 KPGKNRDHYSCYCLSLGLAVSOYSAMTDGSCPLPQHVILGPPYSNLEPIHPLYN 437  
 DB 312 WPSHPDALHAHYFGICGL-----SLMEESGIC-----KVHPALNV 346

RESULT 11  
 PGTL\_RAT STANDARD; PRT; 377 AA.  
 ID PGTL\_RAT  
 AC P53610;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-1996 (Rel. 34, Last annotation update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Geranylgeranyl transferase type I beta subunit (EC 2.5.1.-) (Type I  
 protein geranyl-geranyltransferase beta subunit) (GGTase-I-beta).  
 GN PGGT1B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94148804; PubMed=8106351;  
 RA Zhang F.L., Diehl R.E., Kohl N.E., Gibbs J.B., Giros B.,  
 RA Casey P.J., Omer C.A.;  
 RT "cDNA cloning and expression of rat and human protein  
 geranylgeranyl transferase type-I.";  
 RL J. Biol. Chem. 269:3175-3180(1994).  
 CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM  
 GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL  
 SEQUENCE CYS-ALIPHATIC-ALIPHATIC-X. ACTS ON THE RAC1, RAC2,  
 CC RAP1A AND RAP1B PROTEINS.  
 CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT  
 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 4 PPTB REPEATS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: L24116; AAA17756.1; -.  
 DR InterPro: IPR001330; Prenyltrans.  
 DR Pfam: PF00432; Prenyltrans; 5.



"The Schizosaccharomyces pombe cwg2+ gene codes for the beta subunit of a geranylgeranyltransferase type I required for beta-glucan synthesis." RT  
EMBO J. 12:5245-5254 (1993). RT  
[2] RN  
SEQUENCE FROM N.A. RP  
SPRAIN-972: RC  
Harris D., Wood V., Rajandream M.A., Barrell B.G.; RA  
Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases. RL  
-1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM CC  
GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL C- CC  
A-A-L. IN PARTICULAR IT MODIFIES THE GTP-BINDING COMPONENT OF THE CC  
(1-3)-BETA-D-GLUCAN SYNTHASE. CC  
-1- COPACTOR: BINDS ONE ZINC ION (BY SIMILARITY). CC  
-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. CC  
-1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT CC  
FAMILY. CC  
-1- SIMILARITY: CONTAINS 3 PFTB REPEATS. CC  
----- CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)). CC  
----- CC  
DR EMBL; Z12155; CA478143.1; -. CC  
DR EMBL; AL163071; CAB86347.1; -. CC  
DR PIR; S41686; S41686. CC  
DR HSSP; Q02293; 1FT1. CC  
DR InterPro: IPR001330; Prenyltrans. CC  
DR Pfam; PF00432; Prenyltrans; 4. CC  
KW Transferase: Prenyltransferase; Repeat; Zinc. CC  
FT REPEAT 169 210 PFTB 1. CC  
FT REPEAT 234 275 PFTB 2. CC  
FT REPEAT 282 324 PFTB 3. CC  
FT METAL 260 260 ZINC (BY SIMILARITY). CC  
FT METAL 262 262 ZINC (BY SIMILARITY). CC  
FT METAL 312 312 ZINC (BY SIMILARITY). CC  
SQ SEQUENCE 355 AA; 40023 MW; 811A3CBF0067071 CRC64; CC  
----- CC  
Query Match 12.0%; Score 289.5; DB 1; Length 355; CC  
Best Local Similarity 28.1%; Pred. No. 1.6e-17; CC  
Matches 116; Conservative 47; Mismatches 137; Indels 113; Gaps 16; CC  
----- CC  
QY 59 LEIWRDHIETLPPGLRHHMGPAFVLDANRPWLCYMMVHPALDD--EALDDLENDIID 116  
1 MELIRAHIAFFKRLHLILPFPYEHDCERTVLAFFCLLDLALNTIDDDDKKSMIE 60  
DB 117 FLAR---CODKDGCGYGGPG-----QILPLATTYAANVTLTGSEKALSSIN 161  
DB 61 WIYNNYVTKESGKIKYGFQAYRTGIOPISFEQEPOLAGVFISICCLFLGDN--LSRID 118  
QY 162 RGNLYNFMLOMKDVSAGFR--MHDSGEIDVRASTAIASVSLNIIIDFLAKVCG--DY 216  
DB 119 RDLIKNVEICKTSQGFHRSIAVPSGSDQDRQOLYMATYIASL--LDPSLDPLCSIOY 175  
QY 217 IARCQYEGGIAGEPVAEAGHYFGCLAA--ALIL-----LINEAE-----KVD 257  
DB 176 IKSCQREGEFSLLPYGEAHAGATFCLALMSLILKIMIPNSLNTSNOGYNLMOCYKVE 235  
QY 258 LPSLIGVAVARQGVGEGFOGRTKLVGCGYSFMOGAIAFTOKLITVDKQLASSYSCKR 317  
DB 236 --RLIRMLASRKLSSGGLNRTKNDVDTCYAYW---VLSSSLKL----- 274  
QY 318 PSCGDACSTSYGCTAKSSSAVDYAKFGDFIDQSNQIPLPHNIALQOYIILCSQYLE 377  
DB 275 ----DAL-----PFTIDGGELEKYYLLLHAQHAL 297  
QY 378 GGLRDKPKNRNDHYNSCYCLSLAVSOYSAMTDTSCPLPQ---HYVGPPSNL 427  
DB 298 GGRSKPTGGERPDVLSHSLGLYAMAAYQ-----DDKSPFKVNADIMHISKIINI 344

RESULT 14  
PFTB\_RAT  
ID PFTB\_RAT STANDARD; PRT; 331 AA.  
AC 008603:  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Geranylgeranyl transferase type II beta subunit (EC 2.5.1.-) (RAB  
DE geranylgeranyltransferase beta subunit) (RAB geranyl-  
DE geranyltransferase beta subunit) (RAB GG transferase beta) (RAB GGTase  
DE beta).  
GN RABGGTB OR GGTB.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=93280201; PubMed=8505342;  
RA Armstrong S.A., Seabra M.C., Suedhof T.C., Goldstein J.L.,  
RA Brown M.S.;  
RT "cDNA cloning and expression of the alpha and beta subunits of rat  
RT Rab geranylgeranyl transferase." J.  
RL J. Biol. Chem. 268:12221-12229 (1993).  
RN [2]  
RP CHARACTERIZATION.  
RX MEDLINE=95083621; PubMed=7991565;  
RA Farnsworth C.C., Seabra M.C., Ericsson L.H., Gelb M.H., Glomset J.A.;  
RT "Rab geranylgeranyl transferase catalyzes the geranylgeranylation of  
RT adjacent cysteines in the small GTPases Rab1a, Rab3a, and Rab3a." J.  
RL Proc. Natl. Acad. Sci. U.S.A. 91:11963-11967 (1994).  
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM  
CC GERANYLGERANYL PYROPHOSPHATE TO BOTH CYSTEINES IN RAB PROTEINS  
CC WITH AN -XXCC, -XCXC AND -CCXX C-TERMINAL, SUCH AS RAB1A, RAB3A  
CC AND RAB3A RESPECTIVELY.  
CC -1- COPACTOR: BINDS ONE ZINC ION (BY SIMILARITY).  
CC -1- ENZYME REGULATION: THE ENZYMATIC REACTION REQUIRES THE AID OF A  
CC RAB ESCORT PROTEIN (ALSO CALLED COMPONENT A).  
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT, COLLECTIVELY  
CC CALLED COMPONENT B.  
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN, SPLEEN AND  
CC LIVER. LESS IN THE LUNG, MUSCLE, KIDNEY AND TESTIS; IN THESE  
CC TISSUES, MORE ABUNDANT THAN THE ALPHA SUBUNIT.  
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT  
CC FAMILY.  
CC -1- SIMILARITY: CONTAINS 6 PFTB REPEATS.  
CC ----- CC  
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----- CC  
DR EMBL; L10416; AAA41999.1; -. CC  
DR EMBL; S62097; AAB27019.1; -. CC  
DR PIR; B45977; B45977. CC  
DR HSSP; Q02293; 1FT1. CC  
DR InterPro: IPR001330; Prenyltrans. CC  
KW Transferase: Prenyltransferase; Repeat; Zinc. CC  
FT REPEAT 20 61 PFTB 1. CC  
FT REPEAT 68 109 PFTB 2. CC  
FT REPEAT 116 157 PFTB 3. CC  
FT REPEAT 164 205 PFTB 4. CC  
FT REPEAT 212 253 PFTB 5. CC  
FT REPEAT 260 302 PFTB 6. CC  
FT METAL 238 238 ZINC (BY SIMILARITY). CC  
FT METAL 240 240 ZINC (BY SIMILARITY). CC



Mon Nov 4 12:24:41 2002

us-09-786-675-12.rsp

Page 12

```

Oy      410 DTGSCPLQHWLGPYSNLLEPIHPLY--NVYLDKYHTAYEYFFS 450
          ||      ::||::      | | : |
Db      300 -----LIG--EEQIKPVNPFQMPBEVLGRVNVQPELVS 331

```

Search completed: November 1, 2002, 18:07:53  
Job time : 23 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 1, 2002, 17:09:05 ; Search time 62 Seconds

(without alignments)  
1261.189 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411  
Sequence: 1 MPSPSPPTGDDPPAAMD.....PLYNVLDKHYHAYEFFSEE 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protein:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357.5	56.3	470	10	P93228 Lycopersico
2	1353.5	56.1	470	10	004679 lycopersico
3	1345	55.8	446	10	024448 nicotiana 9
4	832.5	34.5	419	5	09VEV7 drosophila
5	803.5	33.4	401	5	019752 caenorhabditis
6	623.5	25.9	382	3	013782 drosophila
7	531.5	22.0	585	5	09NC76 trypsin
8	343.5	14.2	313	10	09FMP2 arabidopsis
9	342.5	14.2	317	10	080642 arabidopsis
10	336	13.9	317	10	09LHL5 arabidopsis
11	322.5	13.4	376	10	09FPP6 arabidopsis
12	304.5	12.6	347	5	09XZ68 drosophila
13	287	11.9	395	5	024172 drosophila
14	286	11.9	395	5	024173 drosophila
15	244.5	10.1	360	5	018197 caenorhabditis
16	218	9.0	237	11	09CRG6 mus musculus

17	184	7.6	398	3	09Y764 candida alb
18	168.5	7.0	358	10	09LCK1 oryza sativ
19	116	4.8	80	5	09NLV6 leishmania
20	106.5	4.4	514	10	09FRW9 nepenthes a
21	102.5	4.3	410	10	09LFD4 arabidopsis
22	102.5	4.3	553	10	09FVY9 oryza sativ
23	100	4.1	494	10	09FPS0 arabidopsis
24	95.3	4.0	953	5	025412
25	96.5	4.0	502	10	094130 oryza sativ
26	96	4.0	1716	13	091932 cyprinus ca
27	94	3.9	2183	12	091QNH8
28	93.5	3.9	2155	4	075443
29	93.5	3.9	2512	16	010896
30	92.5	3.8	231	11	0921H9
31	92.5	3.8	262	5	09V9S0
32	92.5	3.8	346	16	005805
33	92.5	3.8	585	10	09FPW1
34	92	3.8	365	4	096DL1
35	92	3.8	374	2	0938V4
36	92	3.8	1348	5	09VAD1
37	92	3.8	1392	5	095TQ7
38	92	3.8	1998	5	09V7A5
39	91.5	3.8	791	4	09UFA4
40	91	3.8	347	16	09ZSS1
41	91	3.8	499	2	09AJE4
42	90.5	3.8	271	17	028729
43	90.5	3.8	325	17	09HKA0
44	90.5	3.8	802	4	096PU4
45	90	3.7	608	2	09ZBW6 streptomyce

## ALIGNMENTS

RESULT 1					
P93228	PRELIMINARY:	PRT:	470 AA.		
AC	P93228:				
DT	01-MAY-1997 (TREMBLrel. 03, Created)				
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	PARNESTYL PROTEIN TRANSFERASE SUBUNIT B.				
GN	LEPTB.				
OS	Lycopersicon esculentum (Tomato).				
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:				
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:				
OC	Asteridae: euasterids I: Solanales: Solanaceae: Solanum.				
OX	NCBI_TaxID=4081;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. VENT CHERRY LA1221;				
RX	MEDLINE=97219988; Pubmed=9121446;				
RA	Valovsky S., Trueblood C.E., Callan K.L., Narita J.O., Jenkins S.M.,				
RA	Rine J., Grunsem W.,				
RT	"Plant farnesyltransferase can restore yeast Ras signaling and				
RT	matling."				
RL	Mol. Cell. Biol. 17:1986-1994(1997).				
DR	EMBL: U83708; AAC49666.1; -				
DR	HSSP: 002293; 1FTL				
DR	InterPro: IPR001330; Prenyltrans.				
DR	InterPro: IPR00169; Thiolprot_act.site.				
DR	Pfam: PF00432; Prenyltrans; 5.				
DR	PROSITE: PS00639; THIOLEPROTEINASE_HIS; UNKNOWN_1.				
KW	Transferase.				
SO	SEQUENCE 470 AA; 52220 MW; E5FEDD582B074D3B CRC64;				
Query Match	56.3%; Score 1357.5; DB 10; Length 470;				
Best Local Similarity	57.3%; Pred. No. 1.2e-115;				
Matches: 256; Conservative 68; Mismatches 100; Indels 23; Caps 3;					
OY	25 RLTYQYQKQVKEARVDIYSLGCAAPNPKSIMLELRQDHITLPGRLHMGPARFHL 84				
DB	5 KVTLEDDQWVERRVRREIYDFYISIPNSPSDLIELERKDHFGYLSQGLKRLSPSVL 64				







RX MEDLINE-99069613; PubMed-9851916;  
RA none;  
RT "genome sequence of the nematode *C. elegans*: A platform for  
investigating biology."  
RL Science 282:2012-2018 (1998).  
DR EMBL: 277659; CAB01167.1; -.  
DR HSSP: Q02293; 1FT1.  
DR InterPro: IPR001330; Prenyltrans.  
DR Pfam: PF00432; Prenyltrans; 6.  
SQ SEQUENCE 401 AA; 45093 MW; D767D7C36988D1A CRC64;  
Query Match 33.4%; Score 805.5; DB 5; Length 401;  
Best Local Similarity 38.9%; Pred. No. 3.4e-65;  
Matches 169; Conservative 73; Mismatches 135; Indels 57; Gaps 6;  
QY 22 DLPRLTVQVEQMKVEARVGDYRSL---FGAAPNTKSLIMELMRDOHIEYLPGLRH 77  
DB 18 DDDNFVTSSTQKRIETMLFENYNSLVLEPKTTSDEDLAELTIFRQKHASYLLRYLKN 77  
QY 78 GPARHVIDANRPMLCYMWVHPLALLDEALDDLENDIIDFLARCODKDGSGGPGQLPH 137  
DB 78 PPSYATLDASHSMCYMGVNLKILDAEIPNDVLENTIVFLKSCHEHCGCGPGQLAH 137  
QY 138 LATTYAANVTLTIGSERALSSINGNLNFMLOMKDVSCAFRHHGDEIDVRASYAIS 197  
DB 138 LAPTAAVMCLVSLQKEALRSINRVLFPFLKCKHESGGFYHHEGGEIDMRSAICALA 197  
QY 198 VASLVNILDFAKGVGDYIARCOITYEGGIAGEPPYAEAHGGEYFCGLAALLLNEAEKVD 257  
DB 198 TCEIVGLPMEISNGVAEMITSCSPFGSGEPYTEAHGTYFCVAASVLLNRFILAD 257  
QY 258 LPSLIGVAFRQ-GEVCGFGORTKLVDCGYSEMOGAIAFTOKLITIVDKOLKSSYCK 316  
DB 258 MEGLLRATRRQMRKEGFGORTKLVDCGYSEMOGAIAFTOKLITIVDKOLKSSYCK 306  
QY 317 RPSGEDACSTSYGCTAKKSSAVDYAKFGDFIQOSNOIGPLFNIALOYLILCSQVL 376  
DB 307 -----GRSLKSG-----LPEANMLEEYILVGCOSV 331  
QY 377 EGGLEDRPKNRDHYHSCYCLSGLAISOYSAMTDGSCPLPOHVLGPNLLEPIHPLYN 436  
DB 332 HGGKDRDPKRPVDLYHTCYGLSLGSLVAKOYSLARDGK-----ILGGVNNLAINPVEN 385  
QY 437 VVLDKYNHAYEFS 450  
DB 386 VTIASQFAKEEFT 399

RESULT 6  
013782 PRELIMINARY; PRT; 382 AA.  
AC 013782;  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE PUTATIVE PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (EC 2.5.1.-)  
DE (CAAX FARNESYLTRANSFERASE BETA SUBUNIT)  
OS (CAAX PROTEINS PRENYLTRANSFERASE) (TFASE-BETA).  
GN SPAC17G6.04C.  
OS Schizosaccharomyces pombe (Fission Yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomyces.  
RX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Wood V.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THE BETA SUBUNIT IS RESPONSIBLE FOR PEPTIDE-BINDING.  
CC -!- COFACTOR: CONTAINS A CATALYTIC ZINC ION (BY SIMILARITY).  
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY  
SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT  
CC FAMILY.  
DR EMBL: 299162; CAB16215.1; -.  
DR HSSP: Q02293; 1FT2.  
DR InterPro: IPR001330; Prenyltrans.  
DR Pfam: PF00432; Prenyltrans; 5.  
DR Hypothetical protein; Transferase; Prenyltransferase; Repeat; Zinc.  
FT METAL 253 253 ZINC (BY SIMILARITY).  
FT METAL 255 255 ZINC (BY SIMILARITY).  
FT METAL 316 316 ZINC (BY SIMILARITY).  
SQ SEQUENCE 382 AA; 42188 MW; C3F270593F84203 CRC64;  
Query Match 25.9%; Score 623.5; DB 3; Length 382;  
Best Local Similarity 36.2%; Pred. No. 1.5e-48;  
Matches 152; Conservative 61; Mismatches 144; Indels 63; Gaps 10;  
QY 23 LPRITVQVEQMKVEARVGDYRSLFPGAANTKSLIMELMRDOHIEYLPGLRHMGAPFH 82  
DB 1 MDELSETQVMONETATVATVPLLNG-----ESQSFNLQ-----KHKLITLMKLDPLSPPT 50  
QY 83 VLDANRPMLCYMWVHPLALLDEALDDLENDIIDFLARCODKDGSGGPGQLPHLATTY 142  
DB 51 VLDASRAMYVWELSLAILGK-LDSSVCERALISSVRLKGPSCGCGNGODEHLISTY 109  
QY 143 AAVNTLVTTIGSERALSSINGNLNFMLOMKDVSCAFRHHGDEIDVRASYAISVSLV 202  
DB 110 ASILSLICDSTDVAYSLIERDRLYDMFLSKNPDSFRVNNGESDARSYAAVCVSSLV 169  
QY 203 NI-UDFLKANGVDYIARCOITYEGGIAGEPPYAEAHGGEYFCGLAALLLNEAEKVDPSL 261  
DB 170 GISMDPLPFGTLOWLCKCOTYEGSLGVPYAEAHGGEYFCALAAIALGLGLDLNLTKL 229  
QY 262 IGVAFRQGVGEC-GFGORTKLVDCGYSEMOGAIAFTOKLITIVDKOLKSSYCKRPSG 320  
DB 230 STMVLVQRPDALYGFSGRSKLVDCGYSMWVAGASHVIV----- 267  
QY 321 EDACSTSYGCTAKKSSAVDYAKFGDFIQOSNOIGPLFNH-IALOOYILCSQVLEGG 379  
DB 268 -----ASGYASASHKS-----LPLNLYNPEKLGYLIGCCQSTSG 303  
QY 380 LRDKPGKNRDHYHSCYCLSGLA-VSOYSAMTDGSCPLPOHVLGPNLLEPIHPLYN 437  
DB 304 LRDKPKRPDQYHTCYCLGLSLIAYDYRYHTSDGMSYKPSILHSSLSLL-PAHPITYCV 362

RESULT 7  
09NC76 PRELIMINARY; PRT; 585 AA.  
AC 09NC76;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT.  
OS Trypanosoma brucei brucei.  
OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ISTAR 1.7;  
RA Buchner F.S., Yokoyama K., Nguyen L.N., Grewal A.,  
RA Erdjument-Bromage H., Tempst P., Strickland C.L., Xiao L.,  
RA Van Voorhies W.C., Gelb M.H.;  
RT "Cloning, heterologous expression, and distinct substrate specificity  
of protein farnesyltransferase from Trypanosoma brucei."  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: A930369; AAF73920.1; -.  
DR HSSP: Q02293; 1FT1.  
DR InterPro: IPR001330; Prenyltrans.  
DR Pfam: PF00432; Prenyltrans; 5.  
KW Transferase.  
SQ SEQUENCE 585 AA; 65432 MW; 7568995D868B09 CRC64;  
Query Match 22.0%; Score 531.5; DB 5; Length 585;

Best Local Similarity 29.2%; Pred. No. 7.5e-40;  
Matches 148; Conservative 67; Mismatches 169; Indels 123; Gaps 14;  
OY NTKSIMLEMDHOIEIYLPGLRHMGPAFHVILANRPMILCYMWVHPLALL-----102  
Db 53 NTKSIMLEMDHOIEIYLPGLRHMGPAFHVILANRPMILCYMWVHPLALL-----102  
Db 61 NERGIVHSLNRESHEKYLRLKLEPEYORLNAOPMVMYWTLLQAEMLGTEKLEYOI 120  
OY 103 -----DEALDDLE-----NDIIDLARCQDKDG--126  
Db 121 SODALGEFILSCLOEPVEDEQCGMGSEBGRKSGKMPQCGGNVDFLBRG-DADHTC 179  
OY 127 --GYSGGP-GQLPHLATTYAANTVLTITIGSERLSSINRGNLYNFMLOMGDVGAFPMHD 183  
Db 180 AIFSGGNGQIPHLATSYAGVCSILCGLCPXYLOALPRSAIKRWMLSLCAGDSFPMHI 239  
OY 184 GGEIDVRASYTAISVSLVNIIDFKLAG-----VGDYIARCOYEGGTA-GEPIAEH 236  
Db 240 GGSADIRASVCVAVITTLQLOVDVRSGLLEQEAQFVASCOTIHGGFACGRFASAH 299  
OY 237 GGYTFGGLAALLINEAEKVDLPGLGWAFRG-GVECGFQGRTNKLVDCYSFMOGAA- 294  
Db 300 GAYTQGLAALLIMKRPBELCNNTALRGWLAARGLREGGFNGRTNKLVDSCYAHMWGASH 359  
OY 295 -----IAFTOKLITVDKQKSSYCKRPSGEDACS-----T 326  
Db 360 VILRVGBSLAKITTCGTRKSLTSREMLLDHQAQVDSIMLHPESEFPAWSQHEEKQERA 419  
OY 327 SSYGTAKKSSSAVDYAKFQDFIOOSNOIGPLFHNIALQYILLCQVIL-EGGLRDKPG 385  
Db 420 SREAVLISATPLAASWSSSVPRVDDADGDFYFNQRRLQLYILACQNEBEGMLMKPN 479  
OY 386 KNDHYHSCYCLSGLASO-----YAMTDGSGCP-----LP 417  
Db 480 YPNDPYHTCYLSGMSAQMLOGMQVNRDGRDLSGNSFYAALSRGYIPGRDRSYGIVLP 539  
OY 418 QHVLGPTV-----NLLEPIHPLVNY 437  
Db 540 SDRSGVSSSLHLKSKNCLRFTNFIENI 566  
RESULT 8  
OY Q9FMP2 PRELIMINARY; PRT; 313 AA.  
AC Q9FMP2; 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DB RAB GERANYLGERANYLTRANSEPERASE, BETA SUBUNIT.  
OS Arabidopsis thaliana (mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-COLUMBIA;  
RX MEDLINE=98162728; PubMed=9501997;  
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.  
RT Physically assigned pl clones."  
RL DNA Res. 4:401-414 (1997).  
DR EMBL: AB007727; BAB10039.1; -  
DR HSSP: Q02293; 1FT1.  
DR InterPro: IPR001330; Prenyltrans.  
DR Pfam: PF00432; Prenyltrans; 5.  
KW Transferase  
SQ SEQUENCE 313 AA; 34700 MW; 42588895012A6629 CRC64;  
Query Match 14.2%; Score 343.5; DB 10; Length 313;  
Best Local Similarity 27.1%; Pred. No. 4.8e-23;  
Matches 95; Conservative 60; Mismatches 131; Indels 65; Gaps 8;

OY 58 MLEIMRDOHIEIYLPGLRHMGPAFH-VLDANRPMILCYMWVHPLALLDEALDDLENDII 115  
Db 1 MVOVDKAKHRYILIMAKKK-ESFESVVMHRLNRNGVYWGVLTTDLDDLK-LGCSSEBEVI 58  
OY 116 DFLARCQDKGYSGGGQQLPHLATTYAANTVLTITIGSERLSSINRGNLYNFMLOMKDV 175  
Db 59 SWLMTQHESSGFGFAGNNGHDPHILYTLTAVOIILAFDK---INLIDIGKSSVYAKQNE 115  
OY 176 SGAFRMHDEGEIDVRASYTAISVSLVNIID-FKLAGVGDYIARCOYEGGTAIGEPIAE 234  
Db 116 DGSFSGDMGEIDIRFSYIAICLSILKCDKINVEAAV-KYIVSCNLDGSGFPGAE 174  
OY 235 AHGTFPGGLAALLINEAEKVDLPGLGWAFRGVECGFQGRTNKLVDCYSFMOGAA 294  
Db 175 SHAGQIFCCYGALAITGSLHHYDKDSLGMWMLCERQLKAGGLNGRPEKLADVCYSMWLSS 234  
OY 295 IAFYOKLITVDKQKSSYCKRPSGEDACSTSSYGCTAKKSSAVDYAKFQDFIOOSN 354  
Db 235 LIMDRV-----HVIDKAR-----248  
OY 355 QIGPLFHNIALQYILLCQVILEGLRDKPGKNDHYHSCYCLSGLASOY 405  
Db 249 -----LVKFILDCQDLNCGISDRPDAVDIFHTTGVAGLSLEY 289  
RESULT 9  
OY 080642 PRELIMINARY; PRT; 375 AA.  
AC 080642; 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DB PUTATIVE GERANYLGERANYL TRANSFERASE TYPE I BETA SUBUNIT.  
GN A7639950.  
OS Arabidopsis thaliana (mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV. COLUMBIA;  
RX MEDLINE=20083487; PubMed=10617197;  
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,  
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
RA Cronin L.A., Shen M., VanAken S.E., Umeyan L., Tallon L.J., Gill J.E.,  
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
RA Salzberg S.L., Fraser C.M., Venter J.C.;  
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
RT thaliana."  
RL Nature 402:761-768(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV. COLUMBIA;  
RX Lin X.;  
DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC004218; AAC27846.1; -  
DR HSSP: Q02293; 1FT1.  
DR InterPro: IPR001330; Prenyltrans.  
DR Pfam: PF00432; Prenyltrans; 5.  
KW Transferase  
SQ SEQUENCE 375 AA; 41472 MW; 4D7919F3FA695DF CRC64;  
Query Match 14.2%; Score 342.5; DB 10; Length 375;  
Best Local Similarity 28.1%; Pred. No. 7.8e-23;  
Matches 110; Conservative 60; Mismatches 117; Indels 105; Gaps 15;  
OY 63 RDOHIEIYLPGLRHMGPAFHVILANRPMILCYMWV---HPLALLDEALDDLENDIIDFLA 119  
Db 37 KDRHMLTLEMMYELLPYHYOSQEIINRLTLAHFTISGLHFGARDRVDAKVAKWSLFOA 96

QY 120 ----RCDDKDGCGSGGPG-----QLP-----HLATTAVAANTLVTTIGSERALSS 159  
 DB 97 PPTNRVSLKDKDEFYCGFSRSSOPFIDENGLKHNGSHLSTACALILKVIYCHD--LST 154  
 QY 160 INRGNLVNFMLMDVDSGAFR-MHDGGEIDVRASYTAISVSLVNI--LDFKLAKGVCD 215  
 DB 155 IDSLSLISMTNLQDDGSGFPHIIGETDTRFYVCAALICYMLDSSGCKRESAK--N 211  
 QY 216 VIACQTEGEGIAGEPYEAHGGYTFGGLAAL-----ILINEAK--VDLPISLIGW 264  
 DB 212 YILNCGSYDGGFGLIPSESHGATYCAIASLRIMGYIGVLLSDSSSLIDPSLLNM 271  
 QY 265 VAFQGYECGCGGRTNKLVDGCGYFMOGAIAFTOKLITTYDKLKSYSCKRPSGEDAC 324  
 DB 272 CLQROANDGCGFGGRTNKRPSDTCYAFWICAVL---KLI-----GGDA- 309  
 QY 325 STSYGCTAKKSSAVDYAKRFPFIQSSNIGPLFINIALQOYILLCQVLEGLDKP 384  
 DB 310 -----LIDMKMLRKFLMSC-QSKYGGFSKFP 334  
 QY 385 GKNRDHYHSCYCLSGLAVSQTSAMTDGSCPL 416  
 DB 335 GQLPDLVHSY-----GYTAFSLIEEGGLSPL 361

RESULT 10  
 Q9LHL5 PRELIMINARY: PRT: 317 AA.

ID Q9LHL5  
 AC Q9LHL5:  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE GERANYLGERANYL TRANSFERASE BETA SUBUNIT (GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT, PUTATIVE).  
 GN T21B14.11.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA:  
 RA Kaneo T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S., Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA:  
 RX PubMed=10907853;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety p1, TAC and BAC clones."  
 RT DNA Res. 7:217-221(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA:  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unselid M., Fertmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B., Delgany M., Boutry M., Grievell L.A., Mache R., Pulgomech P., De Simone V., Cholsane N., Artiguenave F., Robert C., Brothier P., Wincker P., Catolico L., Weissenbach J., Saurin W., Queller F., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V., Wurmach E., Drzonek H., Erife H., Jordan N., Bangert S., Wiedemann R., Kranz H., Voas H., Holland R., Brandt P., Nyakatura G., Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B., Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek B., Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Clement J., Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D., Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., de Haan M., Maerise A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,

RA Monfort A., Argilrou A., Flores M., Liguori R., Vitale D., RA Mannheim G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., RA Meyer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J., RA Rooney T., Rizzo M., Walters A., Utterback T., Fujii C.Y., Shea T.P., RA Creasy T.H., Haas B., Maiti R., Mu D., Peterson J., Van Aken S., RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldblyum T.V., RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E., RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T., RA Watanabe A., Yamada M., Yasuda M., Tabata S.  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana."  
 RL Nature 408:820-822(2000).  
 DR EMBL: AP002040; BAB03119.1; JOINED.  
 DR EMBL: AP002063; BAB03119.1; JOINED.  
 DR EMBL: AC069473; AAC51055.1; -.  
 DR HSSP: Q02293; 1FT1.  
 DR InterPro: IPR001330; Prenyltrans.  
 DR Pfam: PF00432; Prenyltrans; 6.  
 KW Transferase.  
 SQ SEQUENCE 317 AA: 35192 MW: 0270555FF230843 CRC64;

Query Match 13.9%; Score 336; DB 10; Length 317;  
 Best Local Similarity 26.4%; Pred. No. 2,4e-22;  
 Matches 90; Conservative 60; Mismatches 129; Indels 62; Gaps 6;

QY 83 VLDAWRWLCYWMYHPLALDEALDDLENDIIDFLARCDDKDGSGGGGOLPHLATTY 142  
 DB 30 VMDLRNMGAVWGLTTLALDK-LGSYSEDEVSWMTQCHESGFGAGNPGHPLVYTL 88  
 QY 143 AAVTLTIGSERALSSINGNLVNFMOKMDVSGAFRMHDGGEIDVRASYTAISVSLV 202  
 DB 89 SAVQIALPDK---LNLIDEXKSNYTAGLONEGSGSIOIWEVDREFIYAIICSL 145  
 QY 203 NILDFKLAKGVGYDIARCQYEGGIAGEPYEAHGGYTFGGLAALLILINEAVDLP 262  
 DB 146 KCLDKIKVKAVDIVYCKMIDGFGGSPGASINAGQIFCCVGLATITGNLHRVDK 205  
 QY 263 GWVAFQGVBC-GPGGRTNKLVDGCGYFMOGAIAFTOKLITTYDKLKSYSCKRPS 321  
 DB 206 WMLCERODYESGLNGRPEKLPDVCYSWVLSLIMIDRV----- 245  
 QY 322 DACSTSSGCTAKKSSAVDYAKRFPFIQSSNIGPLFINIALQOYILLCQVLEGL 381  
 DB 246 -----HWIEKAK-----LYKTIIDSOQMDNGIS 269  
 QY 382 DKPGKNDHYHSCYCLSGLAVSQTSAM-TDTGSCPLPOHVL 421  
 DB 270 DRPSYTVDFHTYFGVAGLSLEPGVKTIDPAVALPVHVI 310  
 RESULT 11  
 Q9PFP6 PRELIMINARY: PRT: 376 AA.  
 ID Q9PFP6  
 AC Q9PFP6:  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE GERANYLGERANYL TRANSFERASE BETA SUBUNIT.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21392285; PubMed=11500541;  
 RA Caldelari D., Sternberg H., Rodriguez-Concepcion M., Grussem M., Valovsky S.;  
 RT "Efficient prenylation by a plant geranylgeranyltransferase-I requires a functional Caal box motif and a proximal polybasic domain";

RL Plant physiol. 126:1416-1429(2001).  
DR EMBL; AF311225; AAG4085.1; -.  
DR HSSP; Q02293; 1FT1.  
DR Interpro; IPR001330; Prenyltrans.  
DR Pfam; PF00432; prenyltrans; 5.  
KW Transference.  
SQ SEQUENCE 376 AA; 41967 MW; 753A7B74210EFB1B CRC64;  
Query Match 13.4%; Score 322.5; DB 10; Length 376;  
Best Local Similarity 27.0%; Pred. No. 5.3e-21;  
Matches 109; Conservative 57; Mismatches 108; Indels 129; Gaps 17;  
QY 57 IMLEL--WRDQHIELT-----PGLRHMG-----AEHVLDANR----- 88  
DB 46 IMLELPHYHQSSEINLTAHTISLHFLGARDRYKVVAKWVLQAFPTNRSVLK 105  
QY 89 PWLCYMWVHLALDEALDDLENDIIDFLARODKDGSGGPGQLPHATTYAAVNTL 148  
DB 106 RMHLMTLWPKVLSPL-----MKNDLKHNGS-----HLASTYCALAIL 146  
QY 149 VTIGSERALSSINGRLNEMLOMKDVSAGFR-MHDGEIDVRASYTAISVASLVNT--- 204  
DB 147 KVIQHD--LSTIDSKSLILIMINLQDDGSFMPHIGGETDLRFVCAAMICVWLDSMSG 204  
QY 205 LDKRLKAGVDYIARCTYEGGIAGEPYAFANHGTYTCGLAAL-----ILLNFAEK 255  
DB 205 MDKESAK--NYILNCCSYDGGFGLPGSSHGATYCAIASRLMGYIGVDLSDNSSS 261  
QY 256 --VDPLSLIGMAVFGQEGCFQGRNTKLVDGYSFMOGAIAFTQKLTITVDKLSKY 313  
DB 262 SIIDPSLLMWLCQROANDGFGCRNKPSDTCYAFWIGAVL-----KLI----- 306  
QY 314 SCRRPSGEDACSTSYGCTAKSSSAVDYAKFGDFITQOSNGIPLPHNIALQOYILCS 373  
DB 307 -----GGDA-----LIDKALKRFLMSC- 324  
QY 374 QVLEGGRLDKRGNRDHYHSCYCLSGLAVSQYSAMDTGSCPL 416  
DB 325 QSKRYGFSKFPGLPLDLYHSY-----GYAFSLLEGGSSPL 362  
RESULT 12  
QYX268 PRELIMINARY; PRT; 347 AA.  
AC QYX268;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE CG18627 PROTEIN (GH25366P).  
GN BETA-GGT-II OR CG18627 OR BETA-GGT-II.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;  
OC Ephyroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RX MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Beos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rochia S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Gioder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., Meleod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Stryker S., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT \*The genome sequence of Drosophila melanogaster.\*;  
RL Science 287:2185-2195(2000).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CANTON S;  
RA Avedisov S.N., Thomas B.J.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Y, CN BW SP;  
RA Stapleton M., Broksstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Munoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003581; AAF51183.1; -  
DR EMBL; AF133269; AAD33042.1; -  
DR EMBL; AY060784; AAL28332.1; -  
DR HSSP; Q02293; 1FT1.  
DR Flybase; FBgn0028970; beta-ggt-II.  
DR Interpro; IPR001330; Prenyltrans.  
DR Pfam; PF00432; prenyltrans; 5.  
KW Transference.  
SQ SEQUENCE 347 AA; 38542 MW; 7BFC74867548E1B4 CRC64;  
Query Match 12.6%; Score 304.5; DB 5; Length 347;  
Best Local Similarity 23.6%; Pred. No. 2.1e-19;  
Matches 90; Conservative 62; Mismatches 136; Indels 93; Gaps 9;  
QY 59 LELMRDQHIEV-----LPPGLRHMGPAFHVLDANRPMVLCYMWVHLALDE 104  
DB 29 LQFWK--HVEYIENHGQEDDEYECMTFLRMSG-----IYGTALDLTMO 73  
QY 105 ALDDLENDIIDFLARCO-DKDGSGGPGQLPHATTYAAVNTLVYIGSERALSSING 163  
DB 74 -LELERKSLIEFVKROGCPNMGFGAFCEGHDPILLTLTSLAIQTLCTYD---ALEEIDRE 129  
QY 164 NLNFMLOMKDVSAGFRMHGGEIDVRASYTAISVASLVNTLD--FLIANGVGYIARCO 221  
DB 130 AVVEFVVGILQOPDGSFGDWKGEVDTRFSCCAVSLITLIMEQTIYERAKVFLVLS 189  
QY 222 TYEGGIGEYFAENHGTYTCGLAALLLDAENVDPRLSLIGWAFRGVCEGCGRTNK 281  
DB 190 QTDGCFSGKPGAESHAALITCCGFFSLTIRHLLDVDKLGWMLCEQRLPSGGLNGRPEK 249  
QY 282 LVDCYGFMOGAIAFQKLTITVDKOLKSSYSCKRPSGEDACSTSYGCTAKSSSAVD 341  
DB 250 LPDVCYMWVLAISLTINGRLHWSSEK----- 276  
QY 342 YAKFGDFITQOSNOIGPLPHNIALQOYILCSQVLEGGRLDKRGNRDHYHSCYCLSGLA 401



Matches	101:	Conservative	55:	Mismatches	122:	Indels	110:	Gaps	14:
QY	85	DANRPMLCYMWHPALALD--EALDDLENDLEIDFL-----ARCQDKD-CGYSGGPGL	135						
		: : :   : : :   : : :   : : :   : : :							
Db	34	DNTRSTIYFPAVCGLDVLSLHVPOLRQDIIIDWIIYGLVYPRDNERKNGCFMCKRANV	93						
		: : :   : : :   : : :   : : :   : : :							
QY	136	P-----HLATTYAAVNTLVLTIGSERALSSINRGNTLYNFMLQMDVSGA	178						
		: : :   : : :   : : :   : : :   : : :							
Db	94	PKTEDAELLCECRNRYQWGHAMTYISLAVLVLTGSD--LSRLDRKSIVDGAANAQKPRESS	151						
		: : :   : : :   : : :   : : :   : : :							
QY	179	F-RHMDGEIDVRSATYTAISVASLVNIIDFLAKVGVDIYIARCQTYEGGIGAGEPYAAHAHG	237						
		: : :   : : :   : : :   : : :   : : :							
Db	152	FSACIDGSEDDRMFYUCCATICTCYMDYMGDVNKKETMFPQETITRSLKRDVGFEQSELGEAHG	211						
		: : :   : : :   : : :   : : :   : : :							
QY	238	GTFEGCALAIIILINAEKYD--LPSLIGVAAFRGVGVCEGFGRTNKLVDGCTYSFWOGAA	294						
		: : :   : : :   : : :   : : :   : : :							
Db	212	GTFECALAAHLHSLQDHLRIADATTVERRMKRLIFRQ--MDGFGGRPNKKPVDTCYSFWIGAS	269						
		: : :   : : :   : : :   : : :   : : :							
QY	235	IAFTOKLITTYDKQLKSSISCKRSPGEGDAGCSISSTGCTAKKSSAVDYAKAFKFFDFLIOGSN	354						
		: : :   : : :   : : :   : : :   : : :							
Db	270	L-----CLIDGFEFLT-----DYAR-----	283						
		: : :   : : :   : : :   : : :   : : :							
QY	355	QIGPLFHNIALQOQYIILCSQVLEGGELRDKPCKNRDRHYSCTYCSLGLAVSQYSAMTDGSC	414						
		: : :   : : :   : : :   : : :   : : :							
Db	284	-----NREFLIISTQDKLIGGFANWPOATPPFPFHTYIGLIGLAF-----TGE-	324						
		: : :   : : :   : : :   : : :   : : :							
QY	415	PLPGHVLGPRYNLEPIHPILYNNVLDKY	442						
		: : :   : : :   : : :   : : :   : : :							
Db	325	--PG-----LSPVNPDSLMSMAAY	341						
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ID	018197	PRELIMINARY;	PRT;	360 AA.
AC	018197;			
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	Y48E1B.3 PROTEIN.			
GN	Y48E1B.3.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	McMurray A.A.;			
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99069613; PubMed=9851916;			
RT	none;			
RT	*Genome sequence of the nematode C.elegans: A platform for			
RT	investigating biology.*;			
RL	Science 282:2012-2018(1998).			
RL	EMBL: Z93393; CAB07699.1; .			
DR	InterPro: IPR001330; Pfam: PF00432; Prentyltrans; 5.			
DR	Pfam: PF00432; Prentyltrans; 5.			
SO	SEQUENCE 360 AA; 40331 MW; C8C7E69CE8716969 CRC64;			

Query Match	10.1%	Score 244.5;	DB 5;	Length 360;
Best Local Similarity	22.8%;	Pred. No. 6.9e-14;		
Matches 91; Conservative	70;	Mismatches 128;	Indels 111;	Gaps 16

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OY 65 QHIEVTEPGLHMGFAFVIEIDANSPWLCYVWVHSLAL---LDEALDDLDLENDIIDIFLARC 121
Db 31 KHIGELHLNVFPQPYTLETTSRNTIFLFASISLDDLGLDELNLTPPERQAVIDMTYGL 90
OY 122 QDKOGSGGSGRG-----QLPHLITTYAANVTLTITIGSERLASSINGNLNYENLQM 172
Db 91 OPTMGNCGFGGSHSCENSICYDENLMLQTTYSALSLALIGDD--LKKVDRKAIILKTYKTA 148
OY 173 KDVSQAFEMHD--GGEIDIVRASYYTIAVSALVN-----ILDF-KLAKGVGDYIARCQTYEG 225

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Db	149	ÖRDNCFCFSSÖGSESDMRFEVCNAVAISHILIDGKEOTIMTKLA----	-GFLQSLNIDG	2040
Oy	226	GIACEPYAEAHGCTYFCJALILILNE--AEKV----	-DLESLGMVAFRGVEGFCGR	279
Db	205	GIGCARGBGSEHGSGTFCCIALSLNSRLMTBEVLTTRDIDRLIMALÖKODI--GFHGRA	262	
Oy	280	NKLVDGCYSFMWGAALIAFTOKLITIVDKLSSYSCKRPSGEBACSTSYSGCTAKKSSA	339	
Db	263	HKPDDSCCAFPMIGA---TLKITL-----	NAVHLNQH---	291
Oy	340	VDYAFEGFDFIQSNOIGPLFHNIALDOYIILLCQSVLEGGJ--	RDRPKRKRDHNSCYL	397
Db	292	-----LRFELMICQHPHIGGFCPKYDEGGSIDLHLYESI	326	
Oy	398	SGLAISOYSAMTIDGSCDPLPOHVLGAPYNNLEPIHPLPVN	437	
Db	327	AAALS-----LLG--EPANVPHPPLSNV	346	

Search completed: November 1, 2002, 18:09:14  
Job time : 69 secs

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